



A new genus *Allodiatrype*, five new species and a new host record of diatrypaceous fungi from palms (Arecaceae)

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Abstract

Diatrypaceous fungi on palms (Arecaceae) in Thailand were collected and identified based on morphological characteristics as well as combined DNA sequence analyses (ITS and TUB2). One new genus *Allodiatrype*, and five new species, *Allocryptovalsa elaeidis*, *Allodiatrype arengae*, *A. elaeidicola*, *A. elaeidis* and *Diatrypella elaeidis* are introduced. A checklist of Diatrypaceae occurring on palms (Arecaceae) and Thai diatrypaceous fungi is also provided.

Keywords – 6 novel taxa – Diatrypaceae – morphology – palm fungi – phylogeny – Thai fungi – Xylariales

Introduction

The ascomycete family Diatrypaceae Nitschke was introduced and typified by *Diatrype* Fr. (Nitschke 1869). Diatrypaceous taxa have a worldwide distribution in aquatic and terrestrial habitats (Chlebicki 1986, Glawe & Jacobs 1987, Carmarán et al. 2006, de Almeida et al. 2016,

Dayarathne et al. 2016, Mayorquin et al. 2016, Senwanna et al. 2017, Shang et al. 2017, 2018, Moyo et al. 2018a). Most genera in Diatrypaceae are wood-inhabiting saprobes (Trouillas et al. 2011, Grassi et al. 2014, Mehrabi et al. 2016, Hyde et al. 2019, Phookamsak et al. 2019); some are plant pathogens causing cankers, dieback and grapevine trunk diseases (caused by *Anthostoma decipiens* (DC.) Nitschke, *Cryptovalsa ampelina* (Nitschke) Fuckel, *Eutypa lata* (Pers.) Tul. & C. Tul., *Eutypella citricola* Speg, *E. microtheca* Trouillas, W.M. Pitt & Gubler, *E. parasitica* R.W. Davidson & R.C. Lorenz (Mostert et al. 2004, Jurc et al. 2006, Luque et al. 2006, 2012, Pitt et al. 2013, Rolshausen et al. 2014, Paolinelli-Alfonso et al. 2015, Mayorquin et al. 2016, Kowalski & Bednarz 2017, Moyo et al. 2018b); and some are endophytes such as *Diatrypella frostii* Peck, *Libertella* Desm. and *Peroneutypa scoparia* (Schwein.) Carmarán & A.I. Romero (de Errasti et al. 2010, Vieira et al. 2011, Grassi et al. 2014).

The number of genera accepted in Diatrypaceae has changed over the years, and four genera have been introduced in the past ten years e.g. *Allocryptovalsa* Senwanna, Phookamsak & K.D. Hyde, *Diatrypasimilis* J.J. Zhou & Kohlm., *Halodiatrype* Dayarathne & K.D. Hyde and *Neoeutypella* M. Raza, Q.J. Shang, Phookamsak & L. Cai (Chalkley et al. 2010, Liu et al. 2015, Dayarathne et al. 2016, Senwanna et al. 2017, Phookamsak et al. 2019). Wijayawardene et al. (2017a) included 17 genera in the family; Phookamsak et al. (2019) introduced the new genus *Neoeutypella*, with two new species, while Hyde et al. (2019) introduced the new species *Diatrypella delonicis* R.H. Perera & K.D. Hyde. Diatrypaceae is, however, relatively poorly studied with regard to potential biotechnological applications, such as the production of enzymes and beneficial secondary metabolites (Ciavatta et al. 2008, Grassi et al. 2014). The only species that have been studied thoroughly for bioactive compounds are the plant pathogenic *Eutypa lata* and *Peroneutypa* (syn: *Eutypella*) *scoparia* (Helaly et al. 2018).

Divergent time estimates and the evolution of major lineages in the Sordariomycetes have indicated that Diatrypaceae has an affinity to many families, such as Graphostromataceae M.E. Barr, J.D. Rogers & Y.M. Ju, Hypoxylaceae DC., Lopadostomataceae Daranag. & K.D. Hyde, Microdochiaceae Hern.-Restr., Crous & J.Z. Groenew., Requiellaceae Boise., and Xylariaceae Tul. & C. Tul. in the order Xylariales at 66–252 Mya, which is the same as the common divergence times of most of fungal families (Samarakoon et al. 2016, Hongsanan et al. 2017). Members of Diatrypaceae mostly have immersed to erumpent or rarely superficial, black or dark brown, eustromatic or pseudostromatic stromata, 8-spored or polysporous asci, hyaline to light brown, allantoid ascospores and a libertella-like asexual morph (Senanayake et al. 2015, Wijayawardene et al. 2017b). The concepts of segregating genera in Diatrypaceae are still rather confused as mentioned in Maharachchikumbura et al. (2016) and Shang et al. (2017, 2018). The placement of species in each genus of Diatrypaceae is very confused with many genera being polyphyletic (Shang et al. 2017, 2018). Hence, it is necessary to use both molecular (mostly based on ITS and TUB2 sequence data) and morphological data for the primary identification and classification of diatrypaceouse taxa.

The number of new microfungi that can be potentially discovered in Thailand is large (Hyde et al. 2018). In this study, we introduce a new genus, five new species, a new combination, new host and new geographical record for Diatrypaceae occurring on palms with morphological and phylogenetic evidence. Detailed descriptions, illustrations, and notes for each taxon are also provided.

Materials & Methods

Collection, isolation, and identification

Fresh materials were collected from Thailand (Chiang Rai, Krabi, and Phang-Nga Provinces) during 2014–2015 on *Arenga pinnata* (Wurmb) Merr., *Brahea armata* S. Watson, *Calamus* L., and *Elaeis guineensis* Jacq. The taxa were identified based on morphological characteristics and DNA sequence data. Isolations and specimen examinations were conducted following the method provided by Konta et al. (2016). The specimens were deposited in the herbarium of Mae Fah Luang University (MFLU) and duplicated in the herbarium of Cryptogams, Kunming Institute of Botany

Academia Sinica (KUN-HKAS). Cultures were deposited in Mae Fah Luang Culture Collection (MFLUCC) at Mae Fah Luang University, Chiang Rai, Thailand. Facesoffungi and Index Fungorum numbers were registered as outlined in Jayasiri et al. (2015) and Index Fungorum (2019).

DNA extraction and amplification (PCR)

Genomic DNA was extracted from fungal mycelium using the Biospin Fungus Genomic DNA extraction Kit (BioFlux, P.R. China) following the manufacturer's protocol. The partial nucleotide genes were subjected to PCR amplification and sequencing of internal transcribed spacer regions and intervening 5.8S rRNA gene (ITS) of the rDNA operon (White et al. 1990), 28S rRNA gene (LSU) (Vilgalys & Hester 1990), 18S ribosomal RNA (SSU) (White et al. 1990), translation elongation factor 1-alpha (*tef1*) (Rehner & Buckley 2005), RNA polymerase II second largest subunit (RPB2) (Liu et al. 1999, Sung et al. 2007) and β -tubulin (TUB2) (Glass & Donaldson 1995, O'Donnell & Cigelnik 1997). For primers and conditions see Table 1.

The total volume of PCR mixtures for amplification were 25 μ l containing 8.5 μ l ddH₂O, 12.5 μ l 2 \times Easy Taq PCR Super Mix (mixture of Easy Taq TM DNA Polymerase, dNTPs and optimized buffer (Beijing Trans Gen Biotech Co., Beijing, P.R. China), 2 μ l of DNA template, 1 μ l of each forward and reverse primers (10 pM). The quality of PCR products was checked on 1% agarose gel electrophoresis stained with 4S green nucleic acid (Life Science Products & Services, Shanghai, P.R. China). Purification and sequencing of PCR products were carried out by Sangon Biotech Co., Shanghai, P.R. China. The resulting fragments were sequenced in both directions with primers above. The DNA sequences generated were analyzed and consensus sequences were computed using SeqMan software.

Table 1 Details of genes/loci with PCR primers and PCR conditions.

Genes/loci	PCR primers (forward/reverse)	PCR conditions
ITS, LSU, SSU, <i>tef1</i>	ITS5/ITS4, LR5/LR0R, NS4/NS1, 983F/2218R	^a ; 95 °C: 30 s, 55 °C: 50 s, 72°C: 30 s (35 cycles); ^c
RPB2	fRPB2-5f/fRPB2-7cR	^b ; 95 °C: 1 min, 54 °C: 2 min, 72 °C: 1.5 min (35 cycles); ^c
TUB2	T1/ Bt2b	^b ; 94 °C: 1 min, 52 °C: 1 min, 72 °C: 1.5 min; ^c

^a Initiation step of 95 °C: 3 min. ^b Initiation step of 95 °C: 5 min. ^c Final elongation step of 72 °C: 10 min and final hold at 4 °C.

Phylogenetic analysis

The new sequences generated in this study were deposited in GenBank (Table 2) even if they were not used in the phylogenetic tree. The sequences generated in this study were analysed with additional sequences obtained from GenBank, based on BLAST searches and the literature (Hyde et al. 2019, Phookamsak et al. 2019). Sequences of the ITS and TUB2 were analysed individually and in combination. Only ITS and TUB2 sequence data were used in the analyses based on previous literature and other gene sequences were deposited in GenBank for future studies. Sequence alignments were carried out with MAFFT v.6.864b (Kato & Standley 2013) and alignments were manually improved where necessary. The single gene datasets were combined using Mega7 (Kumar et al. 2016). Data were converted from fasta to nexus and PHYLIP format with Alignment Transformation Environment online, <https://sing.ei.uvigo.es/ALTER/> (Glez-Peña et al. 2010).

The phylogenetic methods used in this study included maximum likelihood analysis (ML) performed with RAxML GUI v.1.0. (Stamatakis 2006, Silvestro & Michalak 2011) and Bayesian posterior probabilities (BYPP). The latter method was performed at CIPRES using Bayesian analysis on XSEDE (v.3.2.6) as part of the "MrBayes on XSEDE" tool (Huelsenbeck & Ronquist 2001, Miller et al. 2010). MrModelTest v. 2.2 was used to determine the best nucleotide substitution

model settings for the alignment for each data partition of the Bayesian analysis (Nylander 2004). The model of evolution was performed using MrModelTest 2.2 (Nylander 2004) under the Akaike information criterion (AIC). GTR+I+G model was selected as the best-fit models of the combined dataset for maximum likelihood and Bayesian analysis (Nylander 2004). Bayesian posterior probabilities (BYPP) were determined by Markov Chain Monte Carlo sampling (MCMC) in MrBayes on XSEDE v.3.2.6. Six simultaneous Markov Chains were run for 3,000,000 generations and trees were sampled every 1,000th generation. MCMC heated chain was set with a “temperature” value of 0.20. All sampled topologies beneath the asymptote (25%) were discarded as part of a burn-in procedure; the remaining trees (4,502) were used for calculating posterior probabilities in the majority rule consensus tree. BYPP equal to/or greater than 0.90 is given near to each node (Fig. 1). The phylogenetic trees were visualized in Fig Tree v1.4.0 (Rambaut 2006) and edited using Microsoft Office PowerPoint 2010 and Adobe Illustrator CS6 (Adobe Systems, USA). The alignments and respective phylogenetic trees were deposited in TreeBASE (submission ID: 25674).

Results

Phylogenetic analyses

Phylogenetic analyses of combined ITS and TUB2 sequence data based on ML and BYPP analyses indicate that the two tree topologies are similar. The dataset consists of 117 taxa for representative strains of species in Diatrypaceae. The total alignment length comprises 2,570 characters including gaps. The RAxML analysis resulted in a best scoring likelihood tree selected with a final ML optimization likelihood value of -22955.866702 which is represented in Fig. 1. The final likelihood tree was evaluated and optimized under GAMMA model parameters, with 1,547 distinct alignment patterns and 65.11% of undetermined characters or gaps. Bayesian posterior probabilities from MCMC were evaluated with a final average standard deviation of the split frequency of 0.011661.

The phylogram generated from the combined ITS and TUB2 sequence data supports establishment of a new genus, five new species and six new host records of diatrypaceous fungi within Diatrypaceae (Fig. 1). *Allodiatrype* species formed a basal clade to *Neoeutypella*, with *Diatrype enteroxantha* as the sister clade. Of the five new species, *Allocryptovalsa elaeidis* (MFLUCC 15-0707) formed a sister clade with *A. polyspora* (MFLUCC 17-0364, type species) and *A. rabenhorstii* with high bootstrap support within the genus *Allocryptovalsa* (100% ML, 1.00 BYPP). *Allodiatrype arengae* (MFLUCC 15-0713) clustered with *A. elaeidis* with high bootstrap support (100% ML, 1.00 BYPP). *Allodiatrype elaeidis* (MFLUCC 15-0708) clustered with *A. elaeidicola* with 61% ML bootstrap support. *Allodiatrype elaeidicola* (MFLUCC 15-0737) clustered with *A. thailandica* with low bootstrap support. *Diatrypella elaeidis* (MFLUCC 15-0279) is sister to *Diatrypella delonicis* (MFLUCC 15-1014) with low bootstrap support (61% ML). Of the new hosts and geographical records, *Allodiatrype thailandica* (MFLUCC 15-0711) appeared related to the generic type of the genus (MFLUCC 14-1210). Our new isolate of *Diatrypella* (MFLUCC 17-0368) grouped with ex-type strain of *D. heveae* (MFLUCC 15-0274) with high bootstrap support (100% ML, 1.00 BYPP).

Table 2 GenBank accession numbers of sequences used in phylogenetic analyses.

Species	Strains	GenBank accession numbers		References
		ITS	TUB2	
<i>Allocryptovalsa cryptovalsoidea</i>	HVFIG02	HQ692573	HQ692524	Trouillas et al. (2011)
<i>Allocryptovalsa cryptovalsoidea</i>	HVFIG05	HQ692574	HQ692525	Trouillas et al. (2011)
<i>Allocryptovalsa elaeidis</i>	MFLUCC 15-0707	MN308410	MN340296	This study
<i>Allocryptovalsa polyspora</i> ^T	MFLUCC 17-0364	MF959500	MG334556	Senwana et al. (2017)
<i>Allocryptovalsa rabenhorstii</i>	WA07CO	HQ692620	HQ692522	Trouillas et al. (2011)

Table 2 Continued.

Species	Strains	GenBank accession numbers		References
		ITS	TUB2	
<i>Alloccryptovalsa rabenhorstii</i>	WA08CB	HQ692619	HQ692523	Trouillas et al. (2011)
<i>Allodiatrype arengae</i> ^T	MFLUCC 15-0713	MN308411	MN340297	This study
<i>Allodiatrype elaeidicola</i>	MFLUCC 15-0737a	MN308415	MN340299	This study
<i>Allodiatrype elaeidicola</i>	MFLUCC 15-0737b	MN308416	-	This study
<i>Allodiatrype elaeidis</i>	MFLUCC 15-0708a	MN308412	MN340298	This study
<i>Allodiatrype elaeidis</i>	MFLUCC 15-0708b	MN308413	-	This study
<i>Allodiatrype thailandica</i>	MFLUCC 14-1210	KU315392	-	Li et al. (2016)
<i>'Diatrype thailandica'</i>				
<i>Allodiatrype thailandica</i>	MFLUCC 15-0711	MN308414	-	This study
<i>Anthostoma decipiens</i> ^T	IPV-FW349	AM399021	AM920693	Unpublished
<i>Anthostoma decipiens</i> ^T	JL567	JN975370	JN975407	Luque et al. (2012)
<i>Cryptosphaeria eunomia</i> ^T	C1C, CBS 216.87	AJ302417	-	Acero et al. (2004)
<i>Cryptosphaeria eunomia</i> ^T	C5C, CBS 223.87	AJ302421	-	Acero et al. (2004)
<i>Cryptosphaeria ligniota</i>	CBS 273.87	KT425233	KT425168	Acero et al. (2004)
<i>Cryptosphaeria moravica</i>	CBS 244.87	HM164735	HM164769	Trouillas & Gubler (2010)
<i>Cryptosphaeria pullmanensis</i>	ATCC 52655	KT425235	KT425170	Trouillas et al. (2015)
<i>Cryptosphaeria pullmanensis</i>	HBPF24	KT425202	GQ294014	Trouillas et al. (2010)
<i>Cryptosphaeria subcutanea</i>	CBS 240.87	KT425232	KT425167	Trouillas et al. (2015)
<i>Cryptosphaeria subcutanea</i>	DSUB100A	KT425189	KT425124	Trouillas et al. (2015)
<i>Cryptovalsa ampelina</i>	A001	GQ293901	GQ293972	Trouillas et al. (2010)
<i>Cryptovalsa ampelina</i>	DRO101	GQ293902	GQ293982	Trouillas et al. (2010)
<i>Diatrype brunneospora</i>	CNP01	HM581946	HQ692478	Trouillas et al. (2011)
<i>Diatrype bullata</i>	UCDDCh400	DQ006946	DQ007002	Rolshausen et al. (2006)
<i>Diatrype decorticata</i>	1056	KU320621	-	de Almeida et al. (2016)
<i>Diatrype bullata</i>	D6C, CBS 215.87	AJ302422	-	Acero et al. (2004)
<i>Diatrype enteroxantha</i>	HUEFS155114	KM396617	KT003700	de Almeida et al. (2016)
<i>Diatrype enteroxantha</i>	HUEFS155116	KM396618	KT022236	de Almeida et al. (2016)
<i>Diatrype disciformis</i> ^T	D21C, CBS 205.87	AJ302437	-	Acero et al. (2004)
<i>Diatrype disciformis</i> ^T	D7M, GB5815	AJ302423	-	Acero et al. (2004)
<i>Diatrype macowaniana</i>	D15C, CBS 214.87	AJ302431	-	Acero et al. (2004)
<i>Diatrype oregonensis</i>	DPL200	GQ293940	GQ293999	Trouillas et al. (2010)
<i>Diatrype palmicola</i>	MFLUCC 11-0018	KP744439	-	Liu et al. (2015)
<i>Diatrype palmicola</i>	MFLUCC 11-0020	KP744438	-	Liu et al. (2015)
<i>Diatrype polycocca</i>	D16C, CBS 213.87	AJ302432	-	Acero et al. (2004)
<i>Diatrype spilomea</i>	D17C	AJ302433	-	Acero et al. (2004)
<i>Diatrype stigma</i>	DCASH200	GQ293947	GQ294003	
<i>Diatrype stigma</i>	UCD23-Oe	JX515704	JX515670	Úrbez-Torres et al. (2013)
<i>Diatrype undulata</i>	D20C, CBS 271.87	AJ302436	-	Acero et al. (2004)
<i>Diatrype undulata</i>	Olrin324	AY354239	-	Lygis et al. (2004)
<i>Diatrype whitmanensis</i>	CDB011	GQ293954	GQ294010	Trouillas et al. (2010)
<i>Diatrype whitmanensis</i>	DCHES100	GQ293951	GQ294008	Trouillas et al. (2010)
<i>Diatrypella atlantica</i>	HUEFS 136873	KM396614	KR259647	de Almeida et al. (2016)
<i>Diatrypella atlantica</i>	HUEFS 194228	KM396615	KR363998	de Almeida et al. (2016)
<i>Diatrypella banksiae</i>	CPC 29118	KY173402	-	Crous et al. (2013)
<i>Diatrypella delonicis</i>	MFLUCC 15-1014	MH812994	MH847790	Hyde et al. (2019)
<i>Diatrypella delonicis</i>	MFLU 16-1032	MH812995	MH847791	Hyde et al. (2019)
<i>Diatrypella elaeidis</i>	MFLUCC 15-0279	MN308417	MN340300	This study
<i>Diatrypella favacea</i>	Isolate 380	KU320616	-	de Almeida et al. (2016)
<i>Diatrypella frostii</i>	UFMGCB 1917	HQ377280	-	Vieira et al. (2011)
<i>Diatrypella heveae</i>	MFLUCC 17-0368	MF959501	MG334557	Senwana et al. (2017)
<i>Diatrypella heveae</i>	MFLUCC 15-0274	MN308418	MN340301	This study
<i>Diatrypella iranensis</i>	KDQ18	KM245033	-	Mehrabi et al. (2015)
<i>Diatrypella major</i>	Isolate 1058	KU320613	-	de Almeida et al. (2016)
<i>Diatrype oregonensis</i>	CA117	GQ293934	GQ293996	Trouillas et al. (2010)
<i>Diatrypella prominens</i>	DL28A, ATCC 64182	AJ302442	-	Acero et al. (2004)
<i>Diatrype oregonensis</i>	DPL200	GQ293940	GQ293999	Trouillas et al. (2010)
<i>Diatrype prominens</i>		FJ430594	-	Unpublished

Table 2 Continued.

Species	Strains	GenBank accession numbers		References
		ITS	TUB2	
<i>Diatrype prominens</i>	SBen212	KU721868	-	Lawrence et al. (2017)
<i>Diatrypella pulvinata</i>	H048	FR715523	FR715495	de Almeida et al. (2016)
<i>Diatrypella tectonae</i>	MFLUCC 12-0172a	KY283084	-	Shang et al. (2017)
<i>Diatrypella tectonae</i>	MFLUCC 12-0172b	KY283085	KY421043	Shang et al. (2017)
<i>Diatrypella verruciformis</i> ^T	UCROK1467	JX144793	JX174093	Lynch et al. (2013)
<i>Diatrypella verruciformis</i> ^T	UCROK754	JX144783	JX174083	Lynch et al. (2013)
<i>Diatrypella vulgaris</i>	HVFRA02	HQ692591	HQ692503	Trouillas et al. (2011)
<i>Diatrypella vulgaris</i>	HVGRF03	HQ692590	HQ692502	Trouillas et al. (2011)
<i>Eutypa armeniaca</i>	ATCC 28120	DQ006948	DQ006975	Rolshausen et al. (2006)
<i>Eutypa astroidea</i>	E49C, CBS 292.87	AJ302458	DQ006966	Rolshausen et al. (2006)
<i>Eutypa flavovirens</i>	E48C, CBS 272.87	AJ302457	DQ006959	Rolshausen et al. (2006)
<i>Eutypa laevata</i>	E40C CBS 291.87	AJ302449	-	Acero et al. (2004)
<i>Eutypa lata</i> ^T	CBS 290.87	HM164736	HM164770	Trouillas & Gubler (2010)
<i>Eutypa lata</i> ^T	EP18	HQ692611	HQ692501	Trouillas et al. (2011)
<i>Eutypa lata</i> ^T	RGA01	HQ692614	HQ692497	Trouillas et al. (2011)
<i>Eutypa lejoplaca</i>	CBS 248.87	DQ006922	DQ226974	Rolshausen et al. (2006)
<i>Eutypa leptoplaca</i>	CBS 287.87	DQ006924	DQ006961	Rolshausen et al. (2006)
<i>Eutypa maura</i>	CBS 219.87	DQ006926	DQ006967	Rolshausen et al. (2006)
<i>Eutypa microasca</i>	BAFC 51550	KF964566	KF964572	Grassi et al. (2014)
<i>Eutypa sparsa</i>	3802 3b	AY684220	AY684201	Trouillas & Gubler (2004)
<i>Eutypella cerviculata</i> ^T	EL59C	AJ302468	-	Acero et al. (2004)
<i>Eutypella cerviculata</i> ^T	M68	JF340269	-	Arhipova et al. (2012)
<i>Eutypella citricola</i>	HVGRF01	HQ692579	HQ692512	Trouillas et al. (2011)
<i>Eutypella citricola</i>	HVVIT07	HQ692589	HQ692521	Trouillas et al. (2011)
<i>Eutypella leprosa</i>	EL54C, CBS 276.87	AJ302463	-	Acero et al. (2004)
<i>Eutypella leprosa</i>	Isolate 60	KU320622	-	de Almeida et al. (2016)
<i>Eutypella microtheca</i>	ADEL200	HQ692559	HQ692527	Trouillas et al. (2011)
<i>Eutypella microtheca</i>	BCMX01	KC405563	KC405560	Paolinelli-Alfonso et al. (2015)
<i>Eutypella parasitica</i>	CBS 210.39	DQ118966	-	Jurc et al. (2006)
<i>Eutypella semicircularis</i>	MP4669	JQ517314	-	Mehrabi et al. (2016)
<i>Eutypella vitis</i>	UCD2291AR	HQ288224	HQ288303	Úrbez-Torres et al. (2012)
<i>Eutypella vitis</i>	UCD2428TX	FJ790851	GU294726	Úrbez-Torres et al. (2009)
<i>Halodiatrype avicenniae</i>	MFLUCC 15-0953	KX573916	KX573931	Dayarathne et al. (2016)
<i>Halodiatrype salinicola</i> ^T	MFLUCC 15-1277	KX573915	KX573932	Dayarathne et al. (2016)
<i>Kretzschmaria deusta</i>	CBS 826.72	KU683767	KU684190	U'Ren et al. (2016)
<i>Monosporascus cannonballus</i> ^T	CMM3646	JX971617	-	Unpublished
<i>Monosporascus cannonballus</i> ^T	ATCC 26931	FJ430598	-	Unpublished
<i>Neoeutypella baoshanensis</i> ^T	EL51C, CBS 274.87	AJ302460	-	Acero et al. (2004)
<i>Neoeutypella baoshanensis</i> ^T	LC 12111	MH822887	MH822888	Hyde et al. (2019)
<i>Pedumispora rhizophorae</i> ^T	BCC44877	KJ888853	-	Klaysuban et al. (2014)
<i>Pedumispora rhizophorae</i> ^T	BCC44878	KJ888854	-	Klaysuban et al. (2014)
<i>Peroneutypa alsophila</i>	EL58C, CBS 250.87	AJ302467	-	Acero et al. (2004)
<i>Peroneutypa comosa</i>	BAFC 393	KF964568	-	Grassi et al. (2014)
<i>Peroneutypa curvispora</i>	HUEFS 136877	KM396641	-	de Almeida et al. (2016)
<i>Peroneutypa diminutiasca</i>	MFLUCC 17-2144	MG873479	-	Shang et al. (2018)
<i>Peroneutypa diminutispora</i>	HUEFS 192196	KM396647	-	de Almeida et al. (2016)
<i>Peroneutypa kochiana</i>	EL53M	AJ302462	-	Acero et al. (2004)
<i>Peroneutypa longiasca</i>	MFLUCC 17-0371	MF959502	MG334558	Senwana et al. (2017)
<i>Peroneutypa mackenziei</i>	MFLUCC 16-0072	KY283083	KY706363	Shang et al. (2017)
<i>Peroneutypa mangrovei</i>	NFCCI-4246	MG844286	MH094409	Phookamsak et al. (2019)
<i>Peroneutypa rubiformis</i>	MFLUCC 17-2142	MG873477	-	Shang et al. (2018)
<i>Peroneutypa scoparia</i>	MFLUCC 11-0478	KU940151	-	Dai et al. (2016)
<i>Peroneutypa scoparia</i>	MFLUCC 18-1111	MK603519	MK101307	Hyde et al. (2019)
<i>Quaternaria quaternata</i>	EL60C, CBS 278.87	AJ302469	-	Acero et al. (2004)
<i>Quaternaria quaternata</i>	GNF13	KR605645	-	Mehrabi et al. (2016)
<i>Xylaria hypoxylon</i>	CBS 122620	AM993141	KX271279	Peršoh et al. (2009)

Note: Newly generated sequences are in **bold**; ^T denotes the type species of the genus.

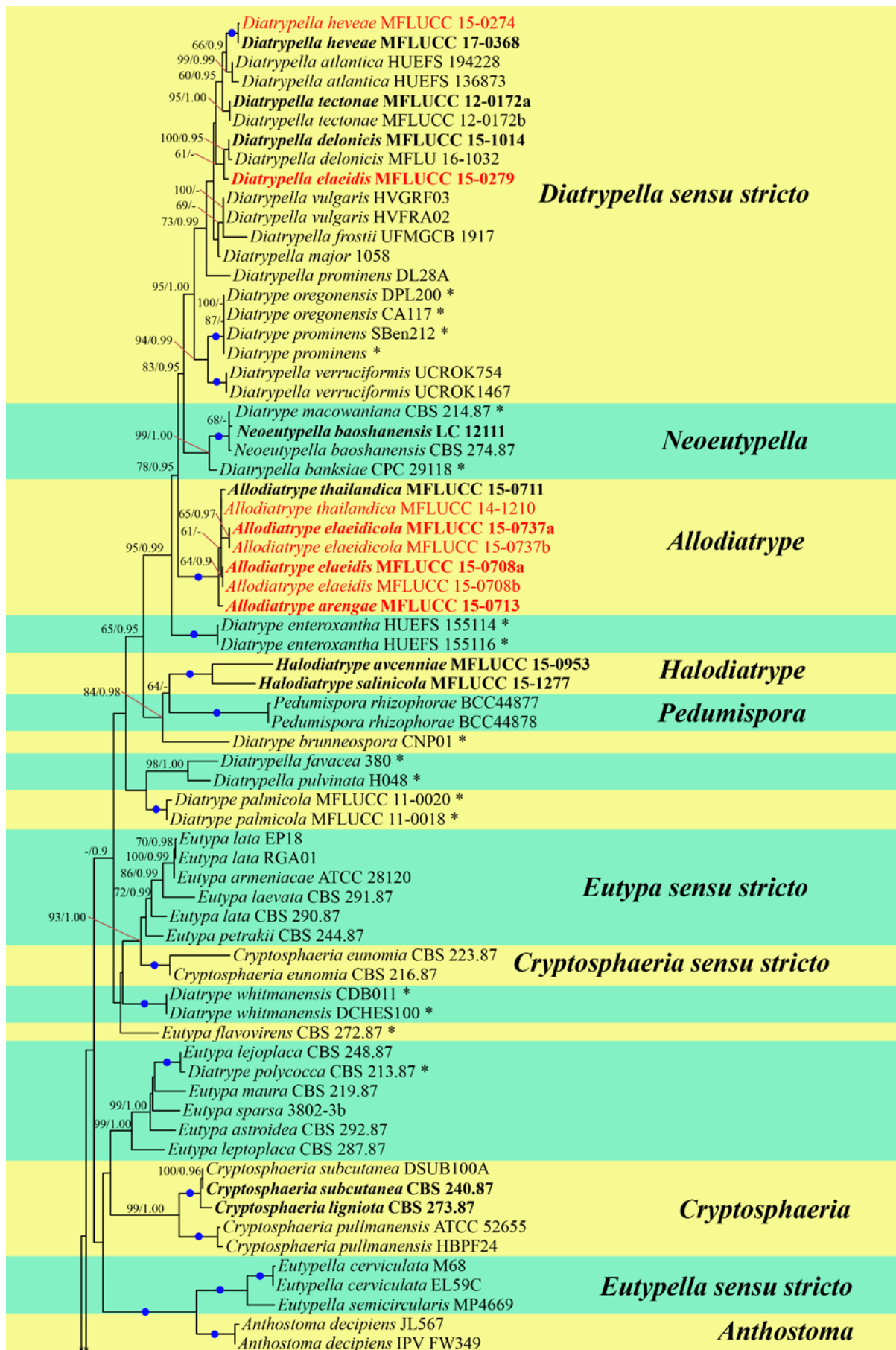


Figure 1 – Bayesian analyses the majority rule consensus tree of selected species in Diatrypaceae generated from combined ITS and TUB2 sequence data. Bootstrap support values for maximum

likelihood (ML) greater than 50%, and Bayesian posterior probabilities (BYPP) greater than 0.90 are given at the nodes. Branches with 100% ML and 1.00 BYPP are shown with a blue dot. Ex-type strains are in bold. Newly generated sequences are in red. Novel taxa are in red bold. The asterisks represent unstable species.

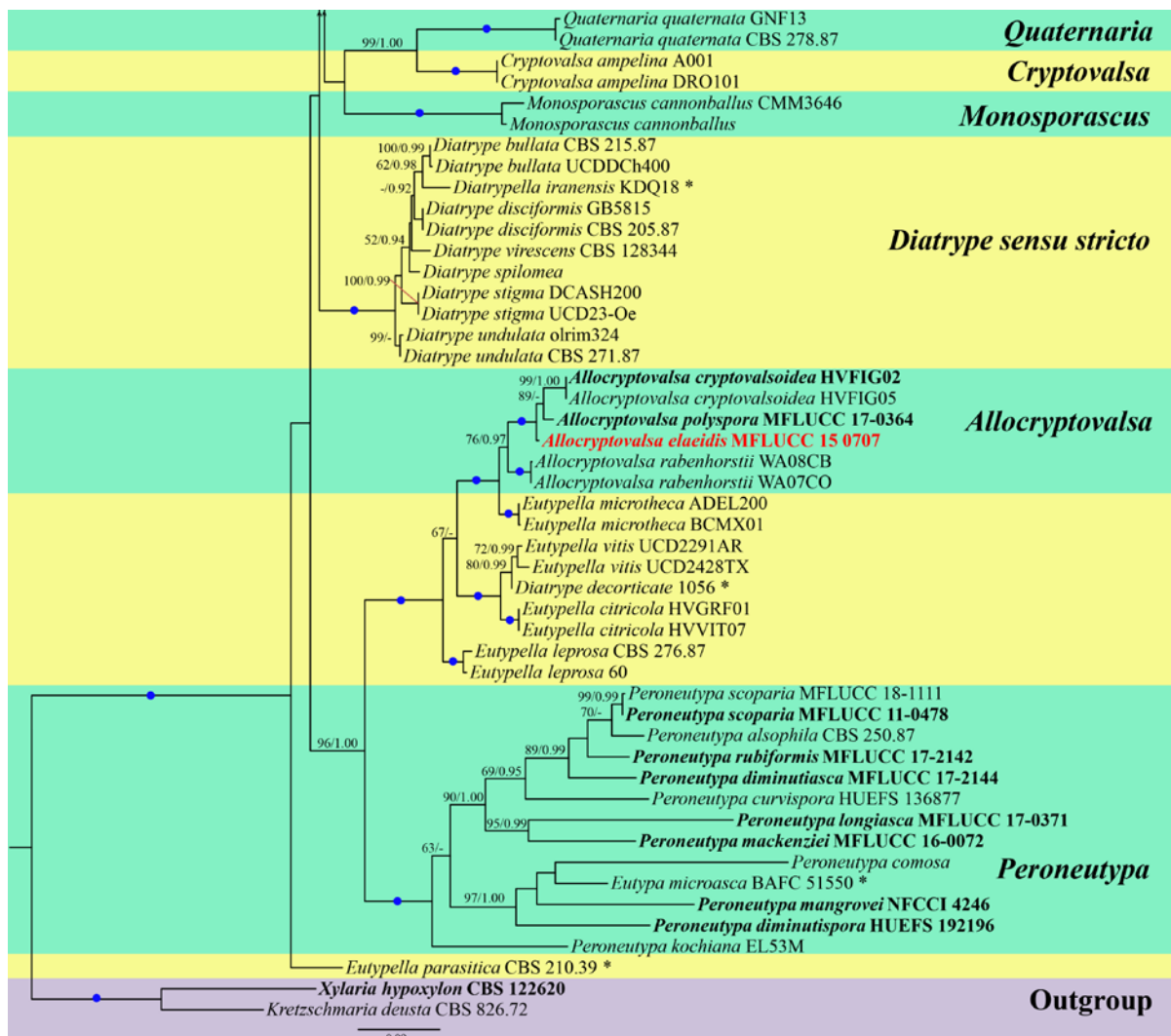


Figure 1 – Continued.

Taxonomy

Allocryptovalsa Senwana, Phookamsak & K.D. Hyde, in Senwana, Phookamsak, Doilom, Hyde & Cheewangkoon, Mycosphere 8(10): 1839 (2017)

Type species – *Allocryptovalsa polyspora* C. Senwana, Phookamsak & K.D. Hyde

Notes – *Allocryptovalsa* was introduced and is typified by *A. polyspora* Senwana, Phookamsak & K.D. Hyde, which was collected from *Hevea brasiliensis* (Senwana et al. 2017). This genus comprises three species, *A. cryptovalsoidea* Trouillas, W.M. Pitt & Gubler ex Senwana, Phookamsak & K.D. Hyde, *A. polyspora* and *A. rabenhorstii* (Nitschke) C. Senwana, Phookamsak & K.D. Hyde (Index Fungorum 2019).

Allocryptovalsa elaeidis Konta & K.D. Hyde, sp. nov.

Index Fungorum number: IF556570, Facesoffungi number: FoF05116

Etymology – Epithet refers to host genus, *Elaeis*

Holotype – MFLU 15-1438

Fig. 2

Saprobic on dead petiole of *Elaeis guineensis* (Arecaceae). Sexual morph – *Stromata* (285–)330–730(–950) μm long, (250–)350–890(–1030) μm wide (\bar{x} = 568 \times 600 μm , n = 20), mostly solitary, sometimes gregarious, surrounded by black circle on host surface, immersed to erumpent in the bark, black, raised, pustulate, dome-shaped, 1–2-ascmata, with umbilicate ostiole appearing on the surface of stroma. *Ascomata* (including neck) 325–460 μm high, 315–515 μm diam. (\bar{x} = 365 \times 400 μm , n = 20), perithecial, immersed in the stroma, covered with the epidermis of plant tissue, delimited by a black zone in host tissues, globose to subglobose, glabrous, ostiole individual, with a short neck. *Ostiolar canal* 180–250 μm high, 160–230 μm diam. (\bar{x} = 250 \times 230 μm , n = 5), sulcate, with periphyses. *Peridium* 25–86 μm wide (\bar{x} = 46 μm , n = 30), composed of two sections, outer layer dark brown, thick-walled cells, arranged in *textura angularis*, inner layer hyaline, thin-walled cells of *textura angularis*. *Hamathecium* composed of 3–13 μm wide (\bar{x} = 6 μm , n = 40), filiform, septate, hyaline, unbranched, paraphyses. *Asci* (including stalks) (55–)68–147(–157) \times 14–26 μm (\bar{x} = 97 \times 18 μm , n = 30), apex-bearing part (1.7–)2–4(–5.5) μm long (\bar{x} = 3 μm , n = 30), polysporous, unitunicate, clavate, with moderately short stalks, stalk-bearing part 35–56 μm long (\bar{x} = 50 μm , n = 10). *Ascospores* (6–)7.5–9(–10.5) \times 2–4 μm (\bar{x} = 9 \times 3 μm , n = 100), overlapping, yellowish to brown, ellipsoidal to cylindrical or elongate-allantoid, aseptate, smooth-walled. Asexual morph – Undetermined.

Geographical distribution – Thailand.

Culture characters – Ascospores germinated on Malt Extract Agar (MEA) within 24 hours. Colonies on MEA, dense but thinner towards the edge, margin diffuse, white of upper surface (Fig. 2q).

Additional sequence data – LSU (MN308401), SSU (MN308419) (MFLUCC 15-0707).

Material examined – THAILAND, Krabi Province, on dead petiole of *Elaeis guineensis* Jacq. (Arecaceae), 3 December 2014, S. Konta, KBM01f (MFLU 15-1438, holotype); ex-type living culture = MFLUCC 15-0707.

Notes – *Allocryptovalsa elaeidis* is morphologically most similar to *A. polyspora*, overlapping in the number of ascomata per stroma, size of ascomata and asci (Senwanna et al. 2017). Although *A. elaeidis* and *A. polyspora* are morphologically similar, the phylogenetic analyses strongly support these collections as two distinct species. *Allocryptovalsa elaeidis* differs from *A. cryptovalsoidea*, *A. polyspora*, and *A. rabenhorstii* in host association, that is *Elaeis guineensis* (*A. elaeidis*), *Ficus carica* (*A. cryptovalsoidea*), *Hevea brasiliensis* (*A. polyspora*), *Robinia* L. and *Vitis vinifera* (*A. rabenhorstii*), respectively (Saccardo 1882, Trouillas et al. 2011, Senwanna et al. 2017). The species of this genus have been reported from Australia, Germany, Thailand, and USA (Saccardo 1882, Trouillas et al. 2011, Senwanna et al. 2017). Comparisons of the nucleotide between *Allocryptovalsa* species are shown in Table 5. Thus, *A. elaeidis* is introduced as the fourth species in *Allocryptovalsa* based on its different morphology coupled with high support values from the phylogenetic analysis (100% ML, 1.00 BYPP, Fig. 1).

Allodiatrype Konta & K.D. Hyde, gen. nov.

Index Fungorum number: IF556641; Facesoffungi number: FoF06299

Etymology – In reference to the morphological resemblance to *Diatrype*

Saprobic on dead petiole of palm (Arecaceae), and on a dead stem of unidentified plants. Sexual morph: *Stromata* scattered or aggregated on the host, erumpent, arising through cracks in the bark, irregularly shaped or circular, orbicular, convex surface, 1–10-ascmata immersed in one stroma, with or without a black stromatic zone. *Ostiole* opening through host bark and appearing as black spots, surrounded with a ring-like, ostiolar opening, composed of an outer layer of dark brown, small, tightly packed, thin parenchymatous cells and an inner layer of yellowish, large, loosely packed, parenchymatous cells. *Ascomata* perithecial, immersed in stromatic tissue, aggregated, brown, globose to sub-globose, narrowing towards the apex and very narrow at the base of ostiolar canal, thin-walled, ostiolate; ostiolar canal, with periphyses, ostiolar opening covered with carbonaceous, black cells; periphyses hyaline, filamentous. *Peridium* comprising an outer layer of yellow-brown, thick-walled cells of *textura angularis* and a thin, inner stratum of

yellow, thick-walled cells of *textura angularis*. *Hamathecium* composed of septate, hyaline paraphyses. *Asci* unitunicate, 8-spored, with long, narrow, thin-walled stalk, with cylindrical, thick-walled, swollen upper portion, apex flat, with J-, cylindrical, conspicuous apical ring. *Ascospores* seriate, hyaline becoming yellowish at maturity, allantoid, unicellular, thin-walled, with small fat globules at each end, smooth-walled. Asexual morph: Undetermined.



Figure 2 – *Allocryptovalsa elaeidis* (MFLU 15-1438, holotype) a Stromata on host substrate. b Close up of stroma. c Section of ascoma. d Peridium. e Ostiolar canal. f Paraphyses. g–j Asci. k–p Ascospores. q Colony on MEA. Bars: a = 500 μ m, b, c = 200 μ m, d, e = 20 μ m, f = 10 μ m, g–j = 50 μ m, k–p = 5 μ m.

Geographical distribution – Thailand.

Type species – *Allodiatrype arengae* Konta & K.D. Hyde

Notes – *Allodiatrype* is introduced to accommodate *Allodiatrype arengae*, *A. elaeidicola*, *A. elaeidis*, and *A.* (syn. *Diatrype*) *thailandica*. *Allodiatrype* is typified by *A. arengae*, which was collected from *Arenga pinnata* (Arecaceae). The morphology of *Allodiatrype* species is closely similar to that of *Diatrype* species. However, *Allodiatrype* differs in having 1–10-ascomata immersed in one stroma, and with or lacking a black stromatic zone, while stromata of *Diatrype* mostly spread over a large area, sometimes covering the host surface. As becomes evident from Fig. 1, strains of both genera appear in distinct clades in a phylogeny based on multiple strains of both genera, thereby justifying the erection of the new genus *Allodiatrype*.

Allodiatrype arengae Konta & K.D. Hyde, sp. nov.

Fig. 3

Index Fungorum number: IF556929, Facesoffungi number: FoF05117

Etymology – Epithet refers to host genus, *Arenga*

Holotype – MFLU 15-1444

Saprobic on petiole of *Arenga pinnata* (Arecaceae). Sexual morph: *Stromata* 690–940 μm long, 370–935 μm wide (\bar{x} = 830 \times 700 μm , n = 10), with well-developed interior, solitary, superficial, black, without black stromatic, glabrous, subglobose to irregular, pustulate, 1–5-ascomata, with umbilicate ostioles appearing on the surface of the stroma. *Ostiole* opening through host bark and appearing as black spots, surrounded with a ring-like structure, composed of an outer layer of dark brown, small, tightly packed, thin parenchymatous cells and an inner layer of yellow, large, loosely packed, parenchymatous cells. *Ascomata* (excluding necks) 250–400 μm high, 240–400 μm diam. (\bar{x} = 340 \times 300 μm , n = 25), perithecial, immersed in the stroma, globose to subglobose, glabrous, ostioles individual, with a short neck. *Ostiolar canal* 100–170 μm high, 70–130 μm diam. (\bar{x} = 130 \times 100 μm , n = 20), cylindrical, sulcate, with periphyses. *Peridium* 12–25 μm wide, (\bar{x} = 20 μm , n = 40), composed of two sections, outer layer of brown to dark brown, thin-walled cells, arranged in *textura angularis*, inner layer of hyaline thin-walled cells of *textura angularis*. *Hamathecium* composed of 3–7 μm wide (\bar{x} = 5 μm , n = 40), septate, hyaline paraphyses. *Asci* (excluding stalks), spore-bearing part (14–)20(–45) \times (4–)6–10(–12) μm (\bar{x} = 30 \times 8 μm , n = 80), apically rounded, with J-apical ring, apex-bearing part (1.5–)3–5(–7.5) μm long (\bar{x} = 4 μm , n = 40), 8-spored, unitunicate, clavate, with long stalks, (28–)34–89(–103) μm long (\bar{x} = 64 μm , n = 60). *Ascospores* (6–)7–10(–12) \times 2–3 μm (\bar{x} = 10 \times 2 μm , n = 120), overlapping, yellowish to light-brown, ellipsoidal to cylindrical or elongate-allantoid, aseptate, smooth-walled. Asexual morph: Undetermined.

Geographical distribution – Thailand.

Culture characters – Ascospores germinated on MEA within 24 hours. Colonies on MEA, white in beginning, dense but thinning towards the edge, margin diffuse, reverse pale yellow in the middle (Fig. 3q).

Additional sequence data – LSU (MN308402), SSU (MN308420), *tef1* (MN525596), RPB2 (MN542886) (MFLUCC 15-0713).

Material examined – THAILAND, Phang-Nga Province, on dead petiole of *Arenga pinnata* (Wurmb) Merr. (Arecaceae), 4 December 2014, S. Konta, PHR01b (MFLU 15-1444, holotype); ex-type living culture = MFLUCC 15-0713.

Notes – *Allodiatrype arengae* was collected from a dead petiole of *Arenga pinnata* from Phang-Nga Province, Thailand. *Allodiatrype arengae* is phylogenetically distinct from its sister species *A. elaeidicola*, *A. elaeidis*, and *A. thailandica* with high statistical support (100% ML, 1.00 BYPP) (Fig. 1). A comparison of the nucleotide between *Allodiatrype* species and *Diatrype disciformis* is given in Table 6. Morphologically, *A. arengae* has superficial stromata lacking a black stromatic zone (Fig. 3a), while *A. elaeidicola* and *A. elaeidis* formed erumpent stromata, arising through the cracks in bark or epidermis with a black stromatic zone (Figs 4a, b, 5a), sometimes it covers the host surface (Fig. 4a, b). Other characters such as ascomata, asci and

ascospores are mostly similar to *A. thailandica*, and their sizes also overlap. Our new strain is also recorded on a different host substrate from other species.

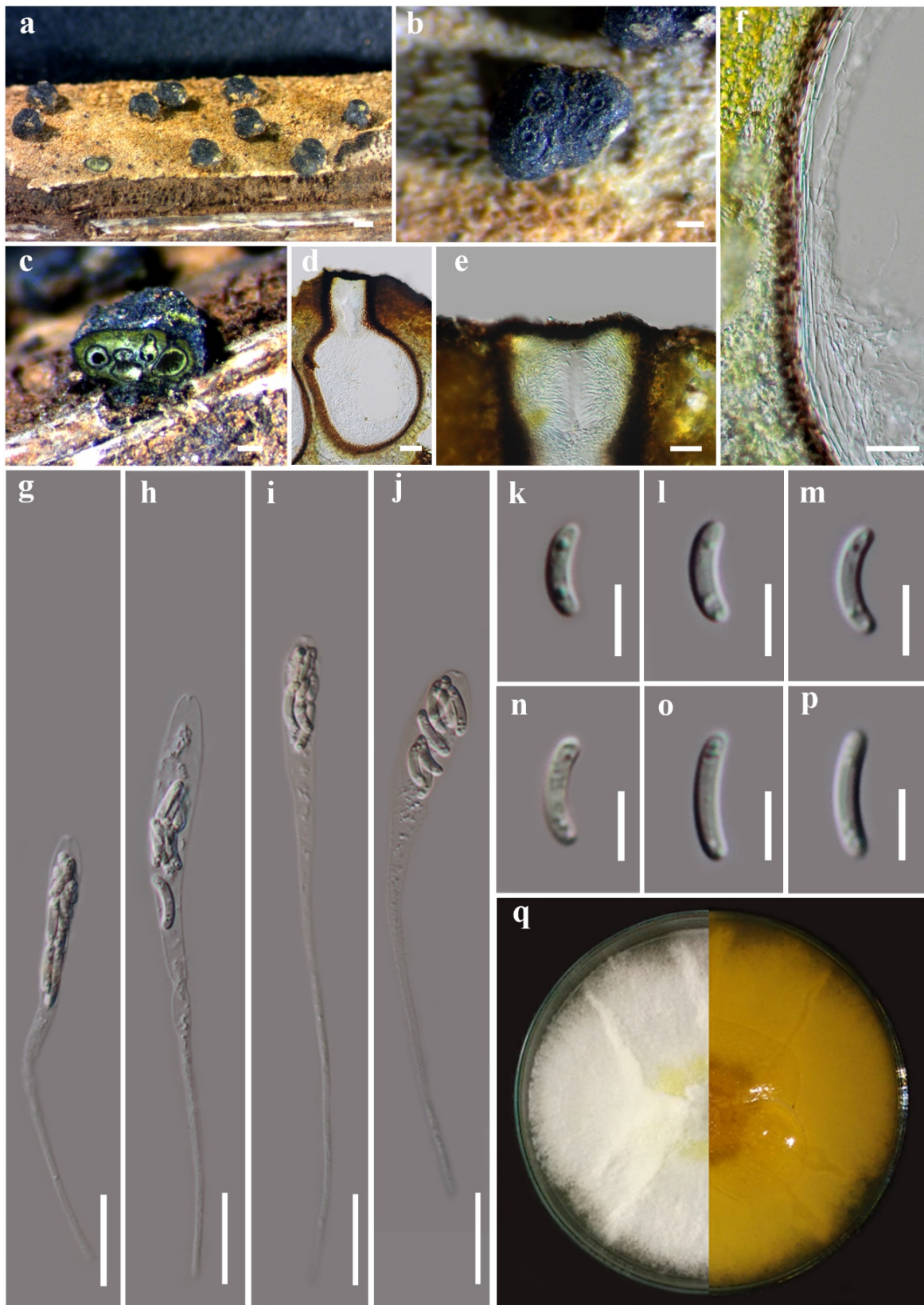


Figure 3 – *Allodiatrype arengae* (MFLU 15-1444, holotype) a Stromata on host substrate. b Close up of stroma (ostiole opening surrounded with a ring-like structure). c, d Section of stroma. e Ostiolar canal. f Peridium. g–j Asci. k–p Ascospores. q Colony on MEA. Bars: a = 500 μ m, b, c = 200 μ m, d, g–j = 50 μ m, e, f = 20 μ m, k–p = 5 μ m.

Allodiatrype elaeidicola Konta & K.D. Hyde, sp. nov.

Fig. 4

Index Fungorum number: IF556930, Facesoffungi number: FoF05118

Etymology – Epithet refers to host genus, *Elaeis*

Holotype – MFLU 15-1468

Saprobic on petiole of *Elaeis guineensis* (Arecaceae). Sexual morph: *Stromata* 1.2–2.8 mm long, 0.96–1.66 mm diam. (\bar{x} = 1.86 × 1.19 mm, n = 15), with well-developed interior, solitary to gregarious, erumpent, black, with black stromatic zone extending down to the host surface, glabrous, irregular in shape, pustulate, multi-ascomata, with umbilicate ostioles appearing on the surface of the stroma. *Ostiole* opening through host bark and appearing as black spots, surrounded with a ring-like structure, composed of an outer layer of dark brown, small, tightly packed, thin parenchymatous cells and an inner layer of yellowish to orange, large, loosely packed, parenchymatous cells. *Ascomata* (excluding necks) 280–430 µm high, 180–435 µm diam. (\bar{x} = 370 × 270 µm, n = 30), perithecial, immersed in the stroma, globose to subglobose, glabrous, ostioles individual, with a short neck. *Ostiolar canal* 120–185 µm high, 60–120 µm diam. (\bar{x} = 140 × 95 µm, n = 30), cylindrical, sulcate, with periphyses. *Peridium* 14–40 µm wide (\bar{x} = 29 µm, n = 30), composed of two section layers, outer part; brown to dark brown, thick-walled cells, arranged in *textura angularis*, inner layer; hyaline, thick-walled cells of *textura angularis*. *Hamathecium* undermined. *Asci* (excluding stalks), spore-bearing part (17–)20–31(–43) × 4–7 µm (\bar{x} = 26 × 6 µm, n = 50), apically rounded, with J-apical ring, apex-bearing part (1.6–)2–3(–5) µm long (\bar{x} = 3, n = 20), 8-spored, unitunicate, clavate, with long stalks, stalk-bearing part (32–)40–60(–76) µm long (\bar{x} = 50 µm, n = 20). *Ascospores* (6.5–)8–10(–11) × 1.5–3 µm (\bar{x} = 9 × 2 µm, n = 100), overlapping, yellowish to brown, ellipsoidal to cylindrical or elongate-allantoid, aseptate, smooth-walled. Asexual morph: Undetermined.

Geographical distribution – Thailand.

Culture characters – Ascospores germinated on MEA within 24 hours and germ tube was produced from end cell. Colonies on MEA, white when beginning, dense but thinner towards edge, margin diffuse, reverse coloration yellow (Fig. 4r).

Additional sequence data – LSU (MN308406), SSU (MN308424), *tef1* (MN525598), RPB2 (MN542889) (MFLUCC 15-0737a); LSU (MN308407), SSU (MN308425), RPB2 (MN542890) (MFLUCC 15-0737b).

Material examined – THAILAND, Phang-Nga Province, on dead petiole of *Elaeis guineensis* Jacq. (Arecaceae), 5 December 2014, S. Konta, PHR10f (MFLU 15-1468, holotype, HKAS95035, Fig. 4); ex-type living culture = MFLUCC 15-0737.

Notes – In the phylogenetic analyses, *Allodiatrype elaeidicola* is related to *A. elaeidis* and *A. thailandica* with low bootstrap support (Fig. 1). However, the taxon is different in having yellow to dark orange inner cells in the stromata (Fig. 4c, d) and thinner walled asci (Fig. 4i), while other species have white to yellow inner cells in the stromata. A comparison of SSU, ITS, TUB2, RPB2 nucleotides to the type species, *A. arengae* shows that *A. elaeidicola* is significantly different from *A. arengae* (SSU, 1/1030 bp (0.09%); ITS, 13/605 bp (2.14%); TUB2, 28/1586 bp (1.76%); RPB2, 3/1139 bp (0.26%) (Table 6).

Allodiatrype elaeidis Konta & K.D. Hyde, sp. nov.

Fig. 5

Index Fungorum number: IF556931, Facesoffungi number: FoF05119

Etymology – Epithet refers to host genus, *Elaeis*

Holotype – MFLU 15-1439

Saprobic on petiole of *Elaeis guineensis* (Arecaceae). Sexual morph – *Stromata* 470–860 µm long, 440–710 µm diam. (\bar{x} = 630 × 550 µm, n = 10), with well-developed interior, solitary to gregarious, erumpent, black, with black stromatic zone on host surface, glabrous, irregular in shape, pustulate, bi- to multi-ascomata, with umbilicate ostioles appearing on the surface of the stroma. *Ostiole* opening through host bark and appearing as black spots, surrounded with a ring-like structure, composed of an outer layer of dark brown, small, tightly packed, thin parenchymatous cells and an inner layer of white to light-yellow, large, loosely packed, parenchymatous cells.

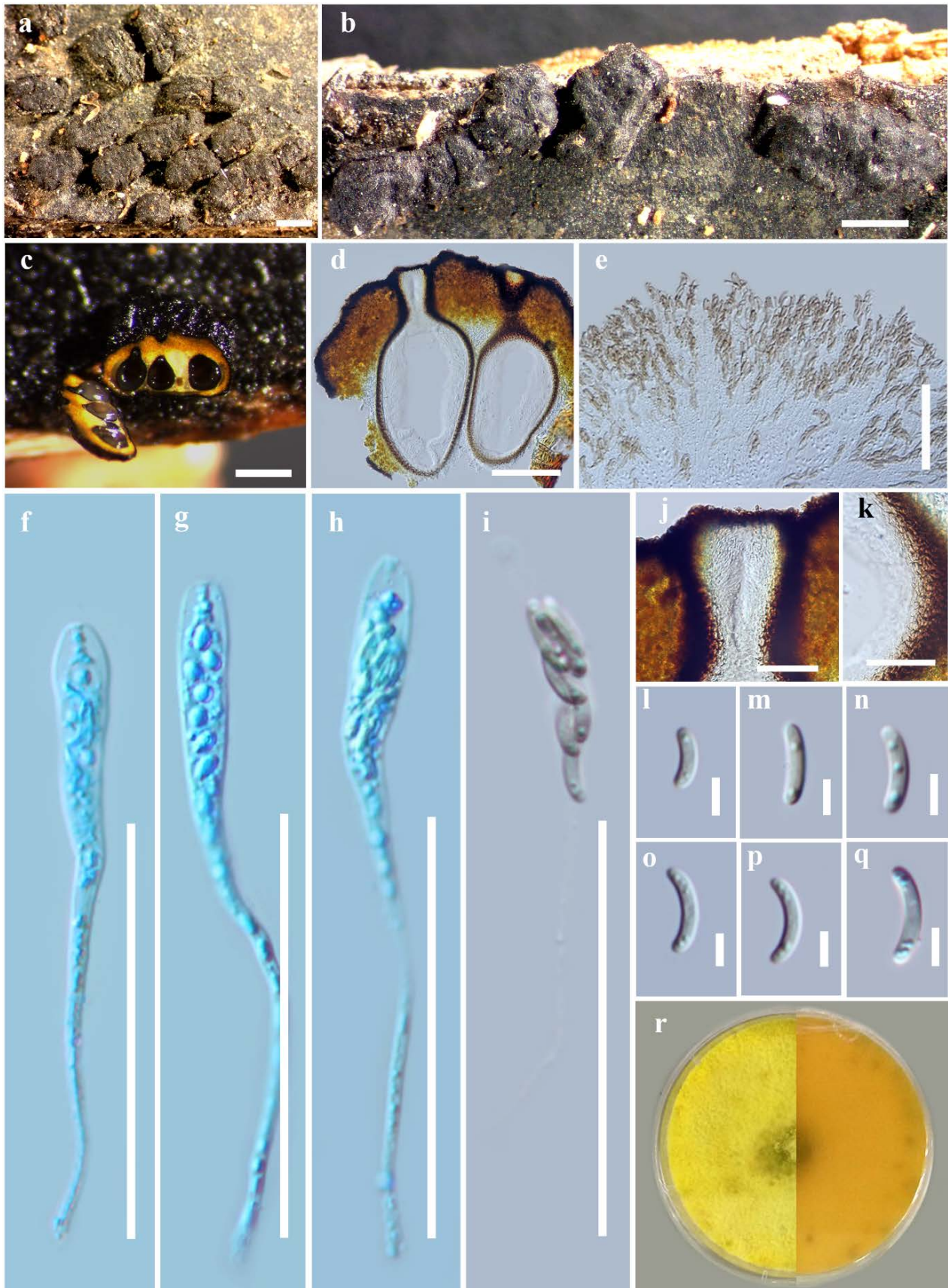


Figure 4 – *Allodiatrype elaeidicola* (MFLU 15-1468, holotype) a Stromata on host substrate. b Close up of stromata (ostiole opening surrounded with a ring-like structure). c, d Section of stroma. e, i Mature asci. f–h Immature asci stained in cotton blue. j Ostiolar canal. k Peridium. l–q Ascospores. r Colony on MEA. Bars: a, b = 1000 μ m, c = 500 μ m, d = 200 μ m, e–k = 50 μ m, l–q = 5 μ m.

Ascomata (excluding necks) 250–350 μm high, 230–300 μm diam. (\bar{x} = 330 \times 280 μm , n = 10), perithecial, immersed in the stroma, globose to subglobose, glabrous, ostioles individual, with a short neck. *Ostiolar canal* 100–130 μm high, 95–115 μm diam. (\bar{x} = 120 \times 110 μm , n = 10), cylindrical, sulcate, with periphyses. *Peridium* 20–40 μm wide (\bar{x} = 30 μm , n = 50), composed of two section layers, outer part; brown to dark brown, thick-walled cells, arranged in *textura angularis*, inner layer; hyaline, thick-walled cells of *textura angularis*. *Hamathecium* composed of 2–7 μm wide (\bar{x} = 4 μm , n = 60), filiform, longer than asci, septate, branch, hyaline, paraphyses. *Asci* (excluding stalks), spore-bearing part (17–)20–30(–39) \times 9–11(–14) μm (\bar{x} = 25 \times 11 μm , n = 60), apically rounded, with J- apical ring, apex-bearing part (1.5–)2–3(–5) μm long (\bar{x} = 3 μm , n = 60), 8-spores, unitunicate, clavate, with moderately long stalks, stalk-bearing part (28–)36–65(–94) μm long (\bar{x} = 50 μm , n = 60). *Ascospores* (6–)8–10(–11) \times 1.5–3) μm (\bar{x} = 9 \times 2 μm , n = 120), overlapping, yellowish to pale-brown, ellipsoidal to cylindrical or elongate-allantoid, aseptate, smooth-walled. Asexual morph – Undetermined.

Geographical distribution – Thailand.

Culture characters – Ascospores germinated on MEA within 24 hours and germ tube was produced from end cell. Colonies on MEA, white at beginning, thinner towards edge, margin diffuse, reverse coloration pale yellow (Fig. 5n).

Additional sequence data – LSU (MN308403), SSU (MN308421), *tef1* (MN525597), RPB2 (MN542887) (MFLUCC 15-0708a); LSU (MN308404), SSU (MN308422), RPB2 (MN542888) (MFLUCC 15-0708b).

Material examined – THAILAND, Krabi Province, on dead petiole of *Elaeis guineensis* Jacq. (Arecaceae), 3 December 2014, S. Konta, KBM01g (MFLU 15-1439, holotype, Fig. 5); ex-type living culture = MFLUCC 15-0708a.

Notes – Multigene phylogenetic analyses (Fig. 1) show that *A. elaeidis* (MFLUCC 15-0708) forms a distinct lineage within the *Allodiatrype* clade and is related to *A. elaeidicola* with 61% ML bootstrap support. *Allodiatrype elaeidis* is morphologically similar to *A. arengae*, *A. elaeidicola* and *A. thailandica* in ascospore size. However, the species differs in its wider asci (9–14 μm). A comparison of ITS, TUB2, RBP2 nucleotides with *A. arengae* shows that *A. elaeidis* is significantly different from *A. arengae* (ITS, 13/621 bp (2.09%); TUB2, 16/1579 bp (1.01%); RBP2, 2/1138 bp (0.17%) (Table 6).

Allodiatrype thailandica (R.H. Perera, Jian K. Liu & K.D. Hyde) Konta & K.D. Hyde, comb. nov.

Index Fungorum number: IF556932, Facesoffungi number: FoF01797

\equiv *Diatrype thailandica* R.H. Perera, Jian K. Liu & K.D. Hyde, Fungal Diversity 78: 1–237. 10.1007/s13225-016-0366-9, [105] (2016)

Description: For original description see Li et al. (2016).

Additional sequence data – LSU (MN308405), SSU (MN308423) (MFLUCC 15-0711).

Material examined – THAILAND, Phang-Nga Province, on dead petiole of *Calamus* sp. (Arecaceae), 6 December 2014, S. Konta, DNH05f (MFLU 15-1442, Fig. 6); living culture = MFLUCC 15-0711.

Notes – According to our analysis in Fig. 1, *Diatrype thailandica* grouped together with *Allodiatrype* species without bootstrap support. This species only has LSU, ITS and SSU sequence data and multigene analysis of ITS and TUB2 sequence data could not be resolved it from the ex-type of *A. elaeidicola*. ITS is unlikely to provide good resolution in Diatrypaceae (Hongsanant et al. 2018). Thus, *Diatrype thailandica* is synonymized under *Allodiatrype*. *Diatrype thailandica* was collected on stems of an unidentified plant from Chiang Rai, Thailand (Li et al. 2016) and in this study, we collected it from *Calamus* (Arecaceae) in Phang-Nga Province. Morphological characters obtained from the fresh specimen is similar to the description provided by Li et al. (2016).

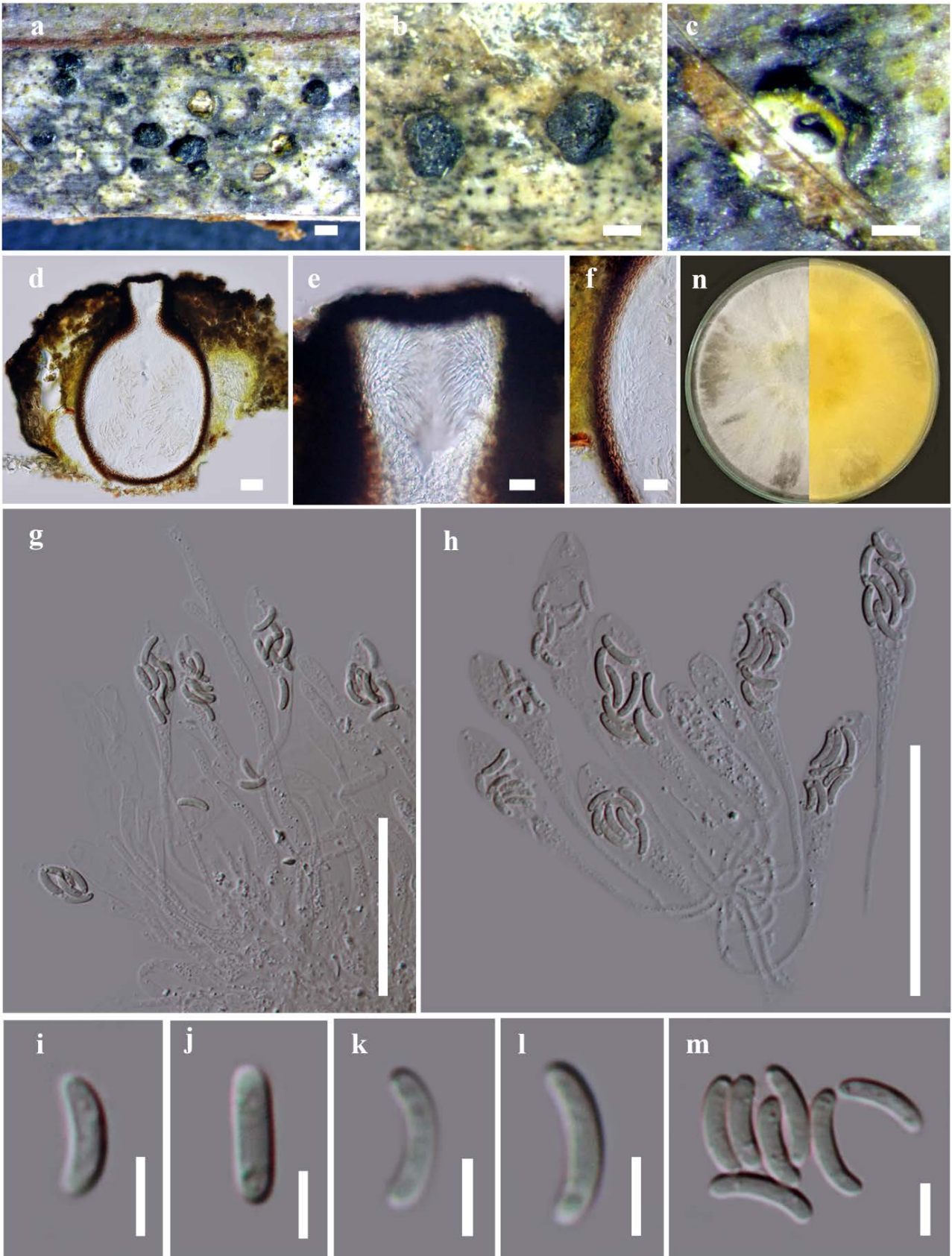


Figure 5 – *Allodiatrype elaeidis* (MFLU 15-1439, holotype) a Stromata on host substrate. b Close up of stromata (ostiole opening surrounded with a ring-like structure). c, d Section of stromata. e Ostiolar canal. f Peridium. g, h Asci. i–m Ascospores. n Colony on MEA. Bars: a, b = 500 μ m, c = 200 μ m, d, g, h = 50 μ m, e, f = 20 μ m, i–m = 5 μ m.

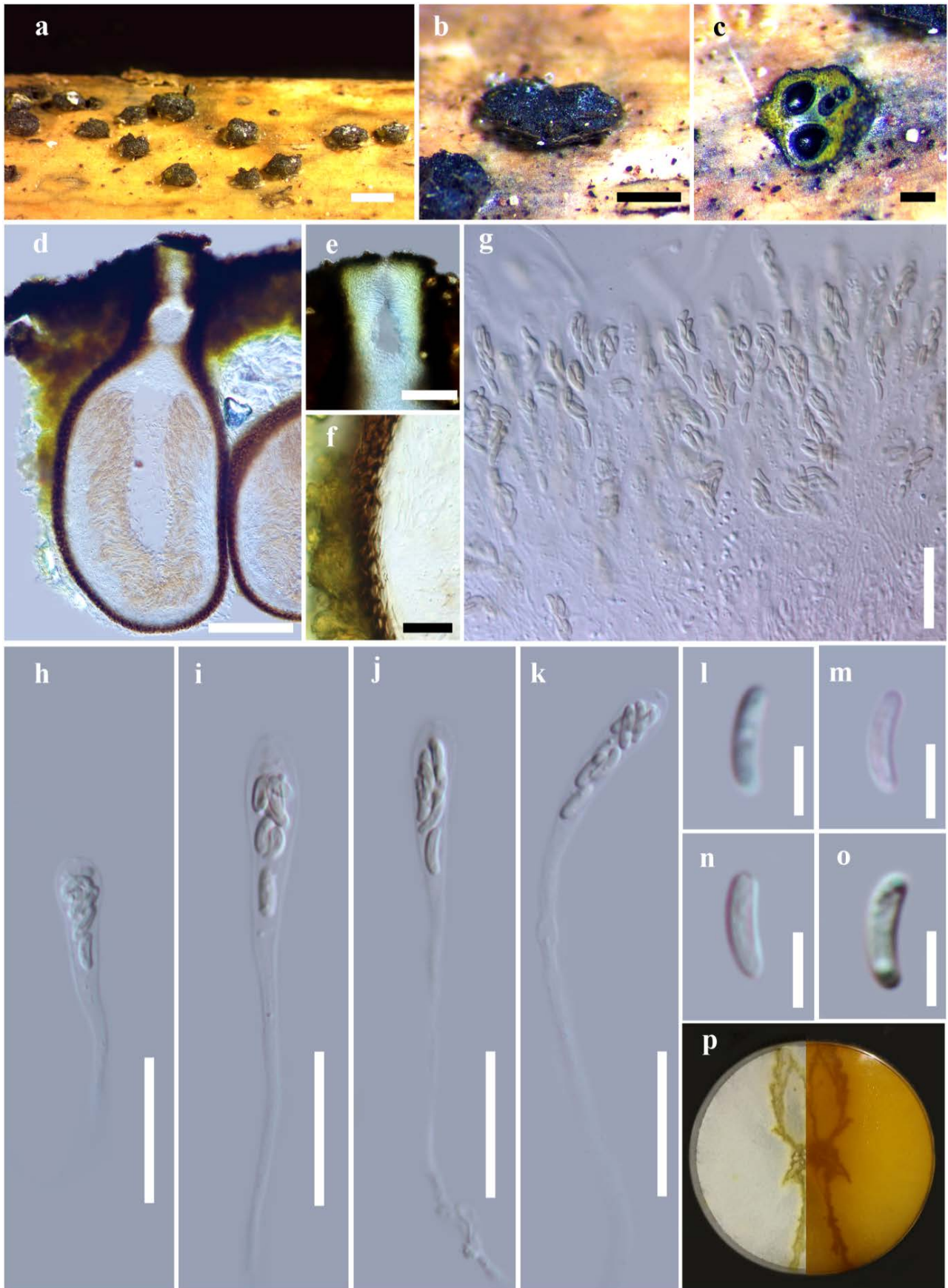


Figure 6 – *Allodiatrype thailandica* (MFLU 15-1442) a Stromata on host substrate. b Close up of stromata. c, d Section of stroma. e Ostiolar canal. f Peridium. g–k Asci. l–o Ascospores. q Colony on MEA. Bars: a = 1000 μm , b = 500 μm , c = 200 μm , e = 50 μm , f, h–k = 20 μm , l–o = 5 μm .

Diatrypella (Ces. & De Not.) De Not

Type species – *Diatrypella verruciformis* (Ehrh.) Nitschke
= *Diatrypella favacea* (Fr.) Ces. & De Not., Sfer. Ital.: 29 (1863))

Notes – The polyphyletic nature of *Diatrypella* has been reported based on the phylogeny of ITS and TUB2 genes (de Almeida et al. 2016, Mehrabi et al. 2016, Senwanna et al. 2017, Shang et al. 2017, Hyde et al. 2019). Currently, 114 epithets are listed under *Diatrypella* (Index Fungorum 2019). Recently an additional species, *Diatrypella delonicis* R.H. Perera & K.D. Hyde. was introduced by Hyde et al. (2019).

Diatrypella heveae Senwanna, Phookamsak & K.D. Hyde, in Senwanna, Phookamsak, Doilom, Hyde & Cheewangkoon, Mycosphere 8(10): 1846 (2017) Fig. 7

Index Fungorum number: IF553859, Facesoffungi number: FoF05121

Saprobic on petiole of *Brahea armata* (Arecaceae). Sexual morph: *Stromata* 660–2155 µm long, 285–860 µm wide (\bar{x} = 1430 × 500 µm, n = 11), with well-developed interior, solitary to gregarious, erumpent in the bark, black, fusiform in shape, pustulate, 1–2-ascomata. *Ascomata* (excluding necks) 70–300 µm high, 90–260 µm diam. (\bar{x} = 181 × 210 µm, n = 20), immersed in the stroma, sub globose to irregular, ostioles individual, with a short neck. *Ostiolar canal* 110–180 µm high, 80–140 µm diam. (\bar{x} = 140 × 110 µm, n = 20), cylindrical, sulcate, with periphyses. *Peridium* 10–35 µm wide (\bar{x} = 22 µm, n = 30), composed of two layers, outer layer of brown, thin-walled cells, arranged in *textura angularis*, inner layer of hyaline, thick-walled cells of *textura angularis*. *Hamathecium* composed of 2–5 µm wide (\bar{x} = 3 µm, n = 30), filiform, longer than asci, septate, hyaline paraphyses. *Asci* (including stalks), spore-bearing part (55–)64–90(–105) × (12–)13–16(–18) µm (\bar{x} = 80 × 15 µm, n = 50), apically rounded, with J- apical ring, apex-bearing part 2–4(–6) µm long (\bar{x} = 3, n = 35), polysporous, unitunicate, clavate, with moderately short stalks, stalk-bearing part 24–36 µm long (\bar{x} = 35 µm, n = 20). *Ascospores* (5–)6–10(–13) × 1–2.5 µm (\bar{x} = 7 × 2 µm, n = 130), overlapping, yellowish to brown, ellipsoidal to cylindrical or elongate-allantoid, aseptate, smooth-walled. Asexual morph: Undetermined.

Geographical distribution – Thailand, Chiang Rai, Wiang Chiang Rung District (Senwanna et al. 2017).

Culture characters – Ascospores germinated on MEA within 24 hours, germ tube produced from end cell. Colonies on MEA smooth, white, dense towards the edge, margin diffuse (Fig. 7v).

Additional sequence data – LSU (MN308409), SSU (MN308427), *tef1* (MN525600), RPB2 (MN542892) (MFLUCC 15-0274).

Material examined – THAILAND, Chiang Rai Province, Mae Chan District, on dead petiole of *Brahea armata* S. Watson. (Arecaceae), 25 November 2014, S. Konta, HR01a (MFLU 15-0020); living culture = MFLUCC 15-0274.

Notes – We collected and illustrated *Diatrypella heveae* (MFLU 15-0020) from Chiang Rai Province, Thailand associated with *Brahea armata* (Arecaceae). This is the second record of this species and the first record of *D. heveae* on a palm; the holotype was collected on rubber from the same province (Senwanna et al. 2017). The phylogenetic results suggested that our strain is the same species, *D. heveae*. The morphological characteristics largely resemble those of *D. heveae* (e.g., the measurements of ascomata, ostiolar canals, peridia, asci, and ascospores, revealed overlapping sizes). However, MFLU 15-0020 differs in having fusiform stromata while the type specimen of *D. heveae* has rounded to irregular stromata and fewer ascomata within a stroma (1–2 versus 4–5) (Senwanna et al. 2017). The sequence data of LSU, SSU, ITS, *tef1*, RPB2, and TUB2 are almost identical to those of the ex-type.

Diatrypella elaeidis Konta & K.D. Hyde, sp. nov. Fig. 8

Index Fungorum number: IF556572, Facesoffungi number: FoF05122

Etymology – Refers to host genus, *Elaeis*

Holotype – MFLU 15-0025

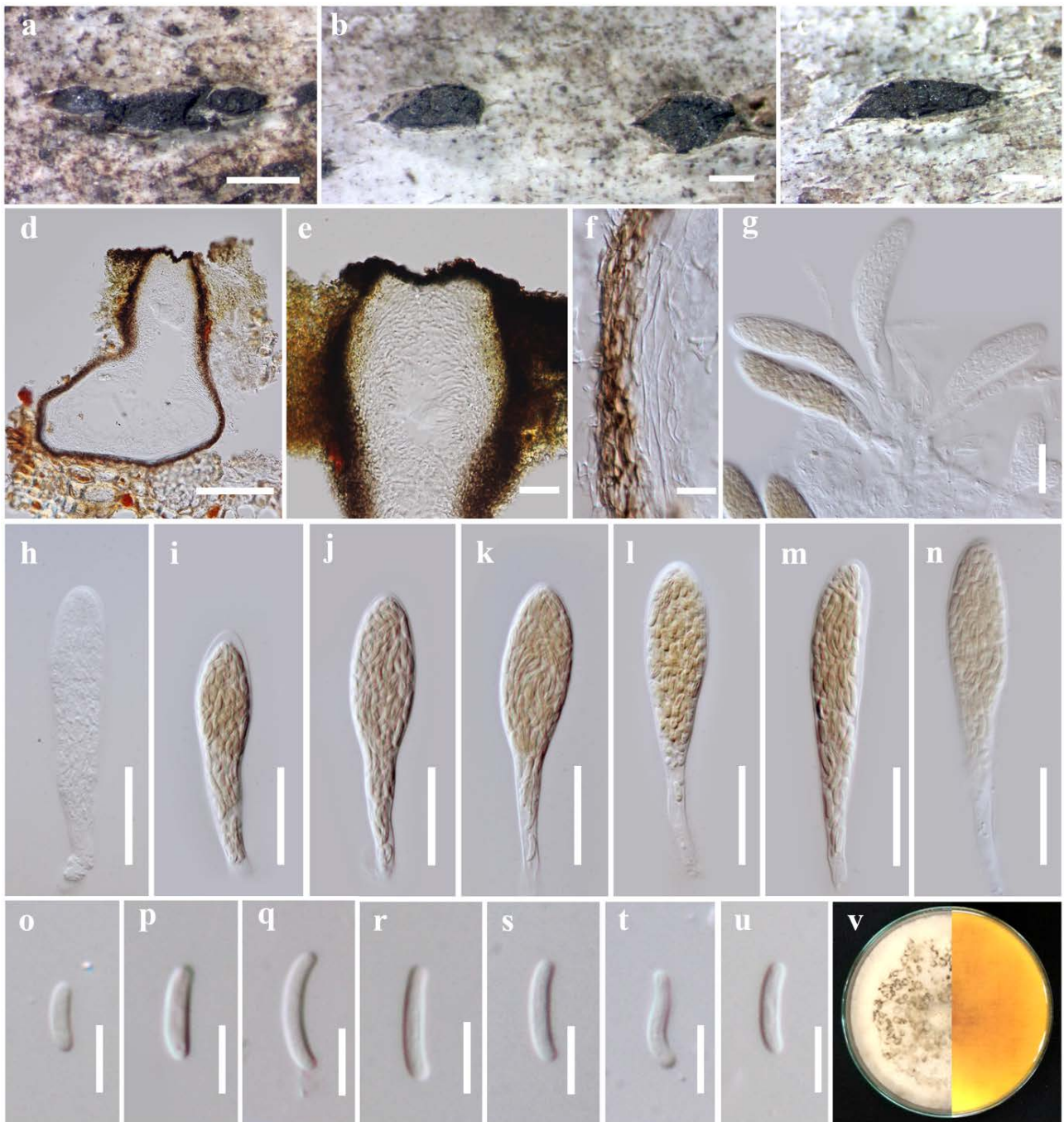


Figure 7 – *DiatryPELLA heveae* (MFLU 15-0020) a Stromata on host substrate. b, c Close up of stromata. d Section of stroma. e Ostiolar canal. f Peridium. g–n Asci. o–u Ascospores. v Colony on MEA. Bars: a = 1000 μm , b, c = 500 μm , d = 50 μm , e, f, g–n = 20 μm , o–u = 5 μm .

Saprobic on petiole of *Elaeis guineensis* (Arecaceae). Sexual morph: *Stromata* 1025–3965 μm long, 285–860 μm wide (\bar{x} = 1950 \times 620 μm , n = 35), with well-developed interior, solitary to gregarious, erumpent, black, glabrous, fusiform or lenticular in shape, pustulate, 1–2-ascomata. *Ascomata* 242–600 μm high, 240–424 μm diam. (\bar{x} = 350 \times 335 μm , n = 25), perithecial, immersed in the stroma, globose to subglobose, ostioles individual, with a short neck. *Ostiolar canal* 100–200 μm high, 70–190 μm diam. (\bar{x} = 140 \times 120 μm , n = 20), cylindrical, sulcate, with periphyses. *Peridium* 22–55 μm wide (\bar{x} = 33 μm , n = 45), composed of two layers, outer part of brown, thick-walled cells, arranged in *textura angularis*, inner layers of hyaline, thick-walled cells of *textura angularis*. *Hamathecium* composed of 2–8 μm wide (\bar{x} = 4 μm , n = 70), filiform, longer than asci, septate, hyaline paraphyses. *Asci* (excluding stalks), spore-bearing part (29–)40–70(–98) \times (7–)11–

15(–17) μm ($\bar{x} = 60 \times 12 \mu\text{m}$, $n = 70$), apically rounded, with J-apical ring, apex-bearing part (0.5–)1–3(–5) μm long ($\bar{x} = 2 \mu\text{m}$, $n = 35$), polysporous, unitunicate, cylindrical, with moderately short stalks, stalk-bearing part (18–)25–40(–57) μm long ($\bar{x} = 33 \mu\text{m}$, $n = 20$). *Ascospores* (3.5–)5–7(–10) \times 1.5–3 μm ($\bar{x} = 6 \times 2 \mu\text{m}$, $n = 130$), overlapping, yellowish to brown, ellipsoidal to cylindrical or elongate-allantoid, aseptate, smooth-walled. Asexual morph: Undetermined.

Geographical distribution – Thailand.

Culture characters – Ascospores germinated on MEA within 24 hours. Colonies on MEA smooth, white, dense towards the edge, margin diffuse (Fig. 8r).

Additional sequence data – LSU (MN308408), SSU (MN308426), *tef1* (MN525599), RPB2 (MN542891) (MFLUCC 15-0279).

Material examined – THAILAND, Chiang Rai Province, Mae Chan District, on dead petiole of *Elaeis guineensis* Jacq. (Arecaceae), 25 November 2014, S. Konta, HR03a (MFLU 15-0025, holotype); ex-type living culture = MFLUCC 15-0279.

Notes – *Diatrypella elaeidis* clearly differs from other species in the genus by its fusiform stroma with 1–2-ascmata immersed in the stroma and their dimensions. *Diatrypella elaeidis* forms a sister clade to *D. delodicis* with bootstrap support of 68% ML, 0.90 BYPP (Fig. 1). However, *D. elaeidis* is distinguished from *D. delodicis* in having black long fusiform stroma, while, *D. delodicis* has pale to dark brown globose to subglobose stroma with a flattened base. Additionally, the number of perithecia per stroma, *D. elaeidis* is less than those in *D. delodicis* (1–2 vs 3–4), asci and hamathecium of *D. elaeidis* are smaller than those of *D. delodicis* (asci; $61 \times 12 \mu\text{m}$ vs $100 \times 18 \mu\text{m}$, hamathecium $4 \mu\text{m}$ vs $9.8 \mu\text{m}$ wide) (Hyde et al. 2019). *Diatrypella delodicis* was found in Chiang Rai on dried seed pods of *Delonix regia* (Fabaceae) (Hyde et al. 2019), while *D. elaeidis* was collected from *Elaeis guineensis*. A comparison of the nucleotide of *D. elaeidis* to *D. delodicis*, *D. heveae*, and *D. verruciformis* (type species) is given in Table 7.

Discussion

Diatrypaceae species are difficult to identify based on morphology due to overlapping phenotypic characters (Glawe & Rogers 1984, Trouillas et al. 2011, Dayarathne et al. 2016, Senwanna et al. 2017, Shang et al. 2017). Many studies have revealed several new hosts of species and have contributed to our knowledge of their geographical distribution (Moyo et al. 2019). In this study, we introduce a new genus and five new species for family Diatrypaceae based on morphology combined with phylogeny. New hosts and new geographical distribution records are also provided. This supports the high novelty of fungal species in Thailand in this family (Hyde et al. 2018). The asexual morphs of Diatrypaceae are usually coelomycetes, but are not generally useful in separating species (Glawe & Rogers 1982, 1984). *Allocryptovalsa* (*Allocryptovalsa* clade, Fig. 1) appears to be a monophyletic group in Diatrypaceae, as was established in previous phylogenetic studies (Senwanna et al. 2017, Hyde et al. 2019). Molecular data are available for *A. cryptovalsoidea*, *A. polyspora* and *A. rabenhorstii* (Trouillas et al. 2011, Senwanna et al. 2017).

In our phylogenetic analyses, a novel genus *Allodiatrype* is introduced. Three novel taxa and a novel combination grouped together but constitute separate lineages (*Allodiatrype* clade, Fig. 1). The strains of *Diatrypella* form a well-resolved clade (Fig. 1). However, in this clade, some strains of *Diatrype* (*D. oregonensis*, *D. prominens*) are placed between *Diatrypella* species. In same case, some strains of *Diatrypella* species such as *D. banksiae*, *D. decorticata*, *D. favacea* and *D. iranensis* often form distinct lineages within Diatrypaceae (Fig. 1). This may be due to lack of TUB2 gene sequences or misidentified species. Hence, fresh collections and sequence data are required to resolve their phylogenetic placement within the family.

Nine genera of Diatrypaceae out of 18 genera (Table 3) have been recorded from palms worldwide (Arecaceae). Of these, seven genera and 20 species (Table 4) have been recorded in Thailand. In addition, our taxa were isolated from dead parts of palms (Arecaceae). They were collected in the same period (November to December 2014) but from different habitats. However, our collection of diatrypaceous fungi are distributed in different hosts as well as different parts of the palms (Arecaceae) and different locations. Moyo et al. (2019) have discussed these aspects and

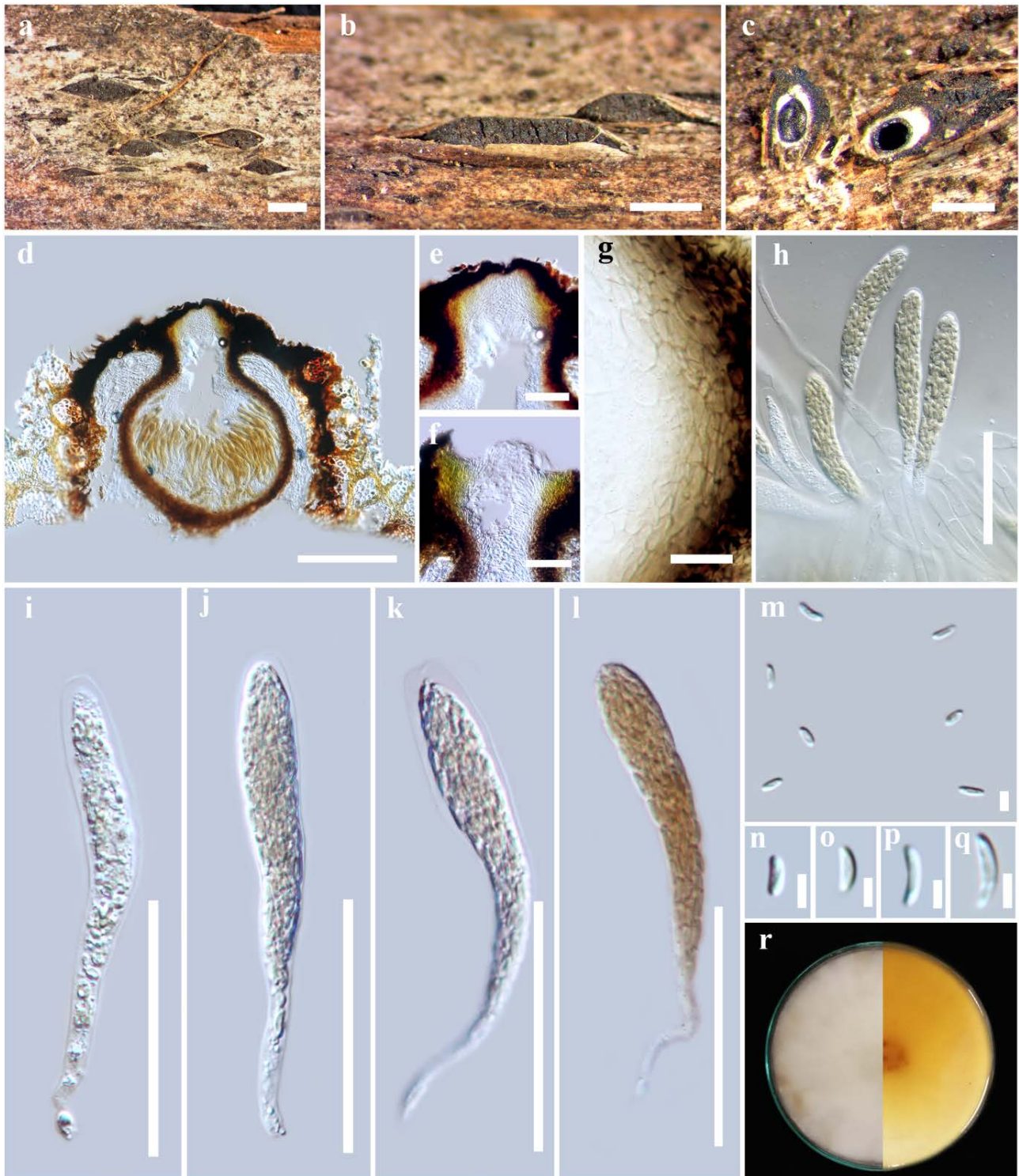


Figure 8 – *Diatrypella elaeidis* (MFLU 15-0025, holotype) a Stromata on host substrate. b Close up of stromata. c, d Sections of stromata. e, f Ostiolar canal. g Peridium. h–l Asci. m–q Ascospores. r Colony on MEA. Scale bars: a, b = 1000 μm , c = 500 μm , d = 200 μm , e, f, h–l = 50 μm , g = 20 μm , m–q = 5 μm .

concluded that broad sampling across the globe might be required to fully comprehend the host associations and distribution of Diatrypaceae.

Our analysis (Fig. 1) showed that *Peroneutypa* forms a monophyletic clade with high statistical support (96% ML, 1.00 BYPP). A putatively named strain, *Eutypa microasca* (BAFC 51550) is placed within this clade but without good statistical support, as shown in the original publication and other studies (Grassi et al. 2014, Shang et al. 2018, Hyde et al. 2019, Phookamsak et al. 2019).

This is just one of many cases showing that the generic concepts of Diatrypaceae are in need of revision. In addition, many genera appear paraphyletic or even polyphyletic in our current phylogeny based on the available material. This situation can only be changed by substantial amounts of fieldwork aimed at collection and culturing of the “missing” taxa, along with careful morphological studies and multi-locus phylogenies.

Table 3 World distribution of Diatrypaceae on palms (Arecaceae).

Genera	Species name	Hosts	Countries	References	
<i>Allocryptovalsa</i>	<i>A. elaeidis</i> Konta & K.D. Hyde.	<i>Elaeis guineensis</i>	Thailand	This study	
<i>Allodiatrype</i>	<i>A. arengae</i> Konta & K.D. Hyde.	<i>Arenga pinnata</i>	Thailand	This study	
	<i>A. elaeidicola</i> Konta & K.D. Hyde.	<i>Elaeis guineensis</i>	Thailand	This study	
	<i>A. elaeidis</i> Konta & K.D. Hyde.	<i>Elaeis guineensis</i>	Thailand	This study	
	<i>A. thailandica</i> (R.H. Perera, Jian K. Liu & K.D. Hyde) Konta & K.D. Hyde. ≡ <i>Diatrype thailandica</i> R.H. Perera, Jian K. Liu & K.D. Hyde	<i>Calamus</i> sp.	Thailand	This study	
	<i>Anthostoma</i>	<i>A. cocois</i> Höhn.	<i>Cocos nucifera</i>	Samoa	Dingley et al. (1981)
	<i>A. yatay</i> Speg.	<i>Cocos yatay</i>	Argentina	Farr (1973)	
<i>Cryptovalsa</i>	<i>C. deusta</i> (Ellis & G. Martin) Petr. ≡ <i>Diatrypella deusta</i> Ellis & G. Martin.	<i>Sabal serrulata</i>	China, U.S.A. (Florida)	Cash (1952), Petrak (1953), Teng (1996)	
	<i>C. protracta</i> (Pers.) De Not. = <i>Diatrypella nitschkei</i> (Fuckel) L.C. Tiffany & J.C. Gilman.	<i>Sabal palmetto</i>	U.S.A. (Florida)	Petrak (1953)	
<i>Diatrype</i>	<i>D. chlorosarca</i> Berk. & Broome.	<i>Archontophoenix alexandrae</i> , <i>Archontophoenix</i> sp., <i>Trachycarpus fortunei</i> , <i>Trachycarpus</i> sp.	China, Hong Kong	Lu et al. (2000), Zhuang (2001), Taylor & Hyde (2003)	
	<i>D. euterpes</i> (Henn.) Rappaz. ≡ <i>Eutypa euterpes</i> Henn.	<i>Euterpe oleracea</i>	Brazil	Rappaz (1987), Mendes et al. (1998)	
	<i>D. palmarum</i> Rick.	<i>Phoenix sylvestris</i>	India	Patil & Patil (1983)	
	<i>D. palmicola</i> Jian K. Liu & K.D. Hyde.	<i>Caryota urens</i>	Thailand	Liu et al. (2015)	
	<i>Diatrype</i> sp.	<i>Rhopalostylis</i> sp.	New Zealand	McKenzie et al. (2004)	
	<i>Diatrypella</i>	<i>D. heveae</i> Senwanna, Phookamsak & K.D. Hyde.	<i>Brahea armata</i>	Thailand	This study
		<i>D. borassi</i> Chona & Munjal.	<i>Trachycarpus fortunei</i> , <i>Archontophoenix alexandrae</i> , <i>Archontophoenix</i> sp.	Australia, Hong Kong	Lu et al. (2000), Zhuang (2001), Taylor & Hyde (2003)
<i>D. caryotae</i> R.K. Verma.		<i>Caryota urens</i>	India	Verma (1996)	
<i>D. elaeidis</i> Konta & K.D. Hyde.		<i>Elaeis guineensis</i>	Thailand	This study	
<i>D. tuberculata</i> Ellis & Catkins ex Ellis & Everh. <i>Diatrypella</i> sp.		<i>Sabal serrulata</i> <i>Rhopalostylis</i> sp.	U.S.A. (Florida) New Zealand	Cash (1952) McKenzie et al. (2004)	
<i>Eutypa</i>	<i>E. rattanicola</i> J. Fröhl. & K.D. Hyde.	<i>Calamus moti</i>	Australia	Fröhlich & Hyde (2000)	
<i>Eutypella</i>	<i>E. arecae</i> (Syd. & P. Syd.) Rappaz.	<i>Areca catechu</i> , <i>Calamus tetradactylus</i> , <i>Calamus</i> sp., <i>Trachycarpus fortunei</i>	China, Hong Kong,	Rappaz (1987), Fröhlich & Hyde (2000), Lu et al. (2000),	

Table 3 Continued.

Genera	Species name	Hosts	Countries	References
			Philippines, Switzerland	Zhuang (2001), Taylor & Hyde (2003)
	<i>E. rehmiana</i> (Henn.) Höhn.	<i>Areca catechu</i> , <i>Areca</i> sp., <i>Calamus</i> sp.	Philippines	Reinking (1918, 1919), Teodoro (1937)
	<i>E. sabalina</i> Cooke.	Areaceae, <i>Chamaerops humilis</i> , <i>Sabal minor</i> , <i>S. palmetto</i> (= <i>Sabal blackburniana</i>), <i>Sabal</i> sp.	Bermuda, China, Georgia, U.S.A. (Alabama, Florida, Louisiana)	Vizioli (1923), Anonymous (1960), Tai (1979), Alfieri et al. (1984), Rappaz (1987), Teng (1996), Glawe & Jones (1989), Zhuang (2001)
	<i>Eutypella</i> sp.	<i>Rhopalostylis</i> sp.	New Zealand	McKenzie et al. (2004)
<i>Peroneutypa</i>	<i>Peroneutypa</i> sp.	<i>Cocos nucifera</i>	Cuba	Urtiaga (1986)

Table 4 Distribution of diatrypaceous fungi on plants in Thailand.

Genera	Species name	Hosts	Collection site (Province)	Collection date	References
<i>Allocryptovalsa</i>	<i>A. polyspora</i> Senwana, Phookamsak & K.D. Hyde.	Dead twig of <i>Hevea brasiliensis</i>	Phayao	29 January 2017	Senwana et al. (2017)
	<i>A. elaeidis</i> Konta & K.D. Hyde.	Dead petiole of <i>Elaeis guineensis</i>	Krabi	3 December 2014	This study
<i>Allodiatrype</i>	<i>A. arengae</i> Konta & K.D. Hyde.	Dead petiole of <i>Arenga pinnata</i>	Phang-Nga	4 December 2014	This study
	<i>A. elaeidicola</i> Konta & K.D. Hyde.	Dead petiole of <i>Elaeis guineensis</i>	Phang-Nga	5 December 2014	This study
	<i>A. elaeidis</i> Konta & K.D. Hyde.	Dead petiole of <i>Elaeis guineensis</i>	Krabi	3 December 2014	This study
	<i>A. thailandica</i> (R.H. Perera, Jian K. Liu & K.D. Hyde) Konta & K.D. Hyde.	Dead petiole of <i>Calamus</i> sp.	Phang-Nga	6 December 2014	This study
	≡ <i>Diatrype thailandica</i> R.H. Perera, Jian K. Liu & K.D. Hyde	Stems of unidentified plant	Chiang Rai	12 March 2015	Li et al. (2016)
<i>Diatrype</i>	<i>D. palmicola</i> Jian K. Liu & K.D. Hyde.	Dead branch of <i>Caryota urens</i>	Chiang Rai	6 September 2010	Liu et al. (2015)
<i>Diatrypella</i>	<i>D. tectonae</i> M. Doilom, Q.J. Shang & K.D. Hyde.	Dead branch of <i>Tectona grandis</i>	Chiang Rai	5 February 2012	Shang et al. (2017)
	<i>D. heveae</i> Senwana, Phookamsak & K.D. Hyde.	Dead twig of <i>Hevea brasiliensis</i>	Chiang Rai	1 November 2016	Senwana et al. (2017)
		Dead petiole of <i>Brahea armata</i>	Chiang Rai	25 November 2014	This study
	<i>D. vulgaris</i> Trouillas, W.M. Pitt & Gubler.	Stems of unidentified plant	Chiang Rai	1 January 2015	Hyde et al. (2017)
	<i>D. delonicis</i> R.H. Perera & K.D. Hyde.	Dried seed pods of <i>Delonix regia</i>	Chiang Rai	10 December 2014	Hyde et al. (2019)
	<i>D. elaeidis</i> Konta & K.D. Hyde.	Dead petiole of <i>Elaeis guineensis</i>	Chiang Rai	25 November 2014	This study
<i>Eutypa</i>	<i>E. flavovirens</i> (Pers.) Tul. & C. Tul.	Decaying twigs	Chiang Rai	15 November 2012	Senanayake et al. (2015)

Table 4 Continued.

Genera	Species name	Hosts	Collection site (Province)	Collection date	References
<i>Halodiatrype</i>	<i>H. avicenniae</i> Dayarathne & K.D. Hyde.	Intertidal decayed wood of <i>Avicennia</i> sp. at a mangrove stand	Phetchaburi	28 August 2015	Dayarathne et al. (2016)
	<i>H. salinicola</i> Dayarathne & K.D. Hyde.	Submerged marine wood	Phang-Nga	7 December 2014	Dayarathne et al. (2016)
<i>Peroneutypa</i>	<i>P. diminutiasca</i> Q.J. Shang, Phookamsak & K.D. Hyde.	Undetermined deadwood	Chiang Mai	27 January 2017	Shang et al. (2018)
	<i>P. longiasca</i> Senwana, Phookamsak & K.D. Hyde.	Dead twig of <i>Hevea brasiliensis</i>	Chiang Rai	1 November 2016	Senwana et al. (2017)
	<i>P. mackenziei</i> Q.J. Shang, Phookamsak & K.D. Hyde.	Undetermined decaying wood	Chiang Rai	22 January 2015	Shang et al. (2017)
	<i>P. rubiformis</i> Q.J. Shang, Phookamsak & K.D. Hyde.	Undetermined deadwood	Chiang Mai	27 January 2017	Shang et al. (2018)
	<i>P. scoparia</i> Carmarán & A.I. Romero.	Dead culms of bamboo	Chiang Rai	16 July 2011	Dai et al. (2016)
		Dead culms of bamboo	Chiang Rai	11 August 2011	Dai et al. (2016)
		Undetermined deadwood	Chiang Mai	27 January 2017	Shang et al. (2018)
		Dieback diseased marine wood	Phetchaburi	11 January 2018	Hyde et al. (2019)

Table 5 Comparison of the nucleotides of *Allocryptovalsa elaeidis* to *A. polyspora*, *A. cryptovalsoidea* and *A. rabenhorstii*.

<i>Allocryptovalsa</i> spp.	LSU	SSU	ITS	TUB2	RBP2	tef1	References
<i>A. polyspora</i> MFLUCC17-0364 ^T	1/823 (0.12%)	-	3/486 (0.62%)	12/516 (2.32%)	-	-	Senwana et al. (2017)
<i>A. cryptovalsoidea</i> HVFIG02	-	-	4/488 (0.81%)	0	-	-	Trouillas et al. (2011)
<i>A. rabenhorstii</i> WA07CO	-	-	23/560 (4.1%)	27/369 (7.31%)	-	-	Trouillas et al. (2011)

Notes – ‘-’ do not have sequence; ‘0’ no base pair similarity; ^T type species; base pair differences included gaps.

Table 6 Comparison of the nucleotides of *Allodiatrype arengae* to all species of *Allodiatrype*, and type species of the genus *Diatrype*.

Species	LSU	SSU	ITS	TUB2	RBP2	tef1	References
<i>A. elaeidicola</i> MFLUCC 15-0737	0	1/1030 (0.09%)	13/605 (2.14%)	28/1586 (1.76%)	3/1139 (0.26%)	0	This study
<i>A. elaeidis</i> MFLUCC 15-0708	0	0	13/621 (2.09%)	16/1579 (1.01%)	2/1138 (0.17%)	0	This study
<i>A. thailandica</i> MFLUCC 14-1210	-	-	9/526 (1.71%)	-	-	-	Li et al. (2016)
<i>A. thailandica</i> MFLUCC 15-0711	0	9/1040 (0.86%)	11/619 (1.77%)	-	-	-	This study
<i>Diatrype disciformis</i> ^T	21/905 (2.32%)	2/894 (0.22%)	56/536 (10.44%)	-	314/1137 (27.6%)	69/957 (7.2%)	Acero et al. (2004)

Notes – ‘-’ do not have sequence; ‘0’ no base pair similarity; ^T type species of *Diatrype*; base pair differences included gaps.

Table 7 Comparison of the nucleotides of *Diatrypella elaeidis* to *D. delodicis*, *D. heveae*, and *D. verruciformis*.

<i>Diatrypella</i> spp.	LSU	SSU	ITS	TUB2	RBP2	tef1	References
<i>D. delonicis</i> MFLUCC 15-1014	-	-	1/600 (0.16%)	7/370 (1.89%)	-	-	Hyde et al. (2019)
<i>D. heveae</i> MFLUCC 15-0274	1/889 (0.11%)	6/1036 (0.57%)	10/603 (1.65%)	15/810 (1.85%)	26/800 (3.25%)	9/954 (0.94%)	This study
<i>D. verruciformis</i> UCROK754	-	-	15/607 (2.47%)	35/367 (9.53%)	-	-	Lynch et al. (2013)

Notes – ‘-’ do not have sequence; ‘0’ no base pair similarity; base pair differences included gaps.

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